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MSPrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Sep 17 16:49:37 1998; MasPar time 10.98 Seconds
425.709 Million cell updates/sec

Tabular output not generated.

Title: >US-08-741-437-1
Description: (1-289) from US08741437.pep
Perfect Score: 2134
Sequence: 1 MSGFSTERAPAFSELYRVF.....CESAGCTVPTDVDRKFMHOKN 289

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 33.562; Variance 136.718; scale 0.245

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	185	8.7	176	19	R98153	Thermococcus litoralis
2	100	4.7	716	10	R55200	Feline zona pellucida
3	97	4.5	345	1	P83149	Probe f10-encoded pro
4	95	4.5	350	8	R42426	Bovine rod transducin
5	91	4.3	354	8	R42424	Rat gustducin alpha s
6	91	4.3	366	3	R12465	HLA-C exon Cb-1.
7	91	4.3	713	11	R60101	Canine zona pellucida
8	91	4.3	715	10	R55198	Canine zona pellucida
9	90	4.2	274	1	P80911	Consensus sequence of
10	90	4.2	1079	28	W38275	Rat kidney cell calci
11	89	4.2	1085	28	W38272	Bovine parathyroid ce
12	88	4.1	138	17	R92524	Pyrodicticum occultum
13	87	4.1	337	2	P70590	Sequence of the human
14	87	4.1	362	2	P70155	Sequence encoded by g
15	88	4.1	366	3	R12466	HLA-C exon Cb-2.
16	87	4.1	535	5	R28411	Protein encoded by cd
17	87	4.1	535	13	R69731	Cyclic-GMP stimulated
18	87	4.1	535	22	W18039	Human brain 61 kDa Ca

19	87	4.1	535	20	W11255	Hippocampus calcium/c
20	87	4.1	738	4	R20192	ADH complex protein (
21	87	4.1	788	3	R13993	A. albertensis membr
22	88	4.1	914	17	R92522	Pyrodicticum occultum
23	87	4.1	1078	28	W38274	Human parathyroid cel
24	87	4.1	1078	20	W11889	Parathyroid calcium r
25	87	4.1	1088	20	W11888	Fungus-infected G.lem
26	87	4.1	1088	14	R70633	Fungus-infected G.lem
27	87	4.1	1088	14	R72398	Glucan lyase 1.
28	87	4.1	1219	24	W25763	Amino acid sequence o
29	88	4.1	3588	7	R34712	Bacillus subtilis str
30	85	4.0	72	15	R86405	Alternatively spliced
31	85	4.0	134	10	R54049	Sequence of the VH re
32	85	4.0	134	20	W01526	Monoclonal antibody 2
33	85	4.0	134	24	W24985	Monoclonal antibody 2
34	86	4.0	362	3	R12464	HLA-B*35 antigen.
35	86	4.0	362	3	R12463	HLA-B*35 exon.
36	86	4.0	379	13	R64159	Human elastase inhibi
37	86	4.0	379	17	R94367	Human elastase inhibi
38	85	4.0	640	3	R15456	Alpha-1,6-glucan-6-g
39	86	4.0	716	12	R60532	Feline zona pellucida
40	86	4.0	1091	14	R72399	Glucan lyase 1.
41	86	4.0	1091	14	R70634	Fungus-infected G.lem
42	85	4.0	1286	2	P70340	Bovine diarrhoea viru
43	83	3.9	362	2	R03142	Sequence of HLA-B*52
44	84	3.9	713	10	R55194	Porcine zona pellucida
45	84	3.9	1356	5	R26999	Novel type III RIK en

ALIGNMENTS

RESULT	1	Query Match	8.7%	Score 185;	DB 19;	Length 176;
ID	R98153	Standard: Protein; 176 AA.	Best Local Similarity 36.9%;	Pred. No. 3.58e-07;		
AC	R98153	Matches 31; Conservative 20; Mismatches .30; Indels 3; Gaps 3;				
DI	06-JAN-1997	(first entry)				
DE	Thermococcus litoralis	(first entry)				
KW	Inorganic pyrophosphatase; pyrophosphate phosphohydrolase; Ppase;					
OS	Thermococcus litoralis strain NS-C (DSM 5473).					
PN	W09612798-AL.					
PD	02-MAY-1996.					
PF	23-OCT-1995; U13662.					
PR	25-OCT-1994; US-329721.					
PA	(NEMO) NEW ENGLAND BIOLABS INC.					
PI	Lennox T. Sears LE, Slatko BE;					
DR	WPI: 96-230599/23.					
DR	N-PSDB: T30073.					
PT	Thermococcus litoralis					
PS	Claim 1: Page 57; 85pp; English.					
CC	The thermococcus litoralis has a subunit mol. wt. of 20-21 kDa. It is					
CC	active after 4 hr incubation at 100 deg C and retains 100% of its					
CC	(T30073) into an expression vector allows prodn. of recombinant					
CC	Ppase in transformed host cells. The Ppase may be used to					
CC	eliminate problems of pyrophosphorylation in reactions conducted					
CC	at temp. above 37 deg C; esp. when an accumulation of					
CC	pyrophosphates could be a problem, e.g. thermal cycling processes					
CC	utilising DNA polymerases.					
SO	Sequence 176 AA;					
DB	66 dddpfdmvmeyrlypypvleazrpigfkmidsqdkykvlaevpepyfndwdisdv 125					
QY	116 dndpfdmvmeyrlypypvleazrpigfkmidsqdkykvlaevpepyfndwdisdv 175					
DB	126 -p-ka-fideiahhfgyrykylgk 146					
QY	176 krlkpgyleatvdmrerrkypvdkg 199					

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DR      N-PSDB, N80603.
PT      Restriction fragment length polymorphism genotyping test -
PT      for chickens, using erythrocyte DNA fragments and hybridisation
PS      probe derived from histocompatibility complex antigen.
PS      Disclosure; p. French.
CC      Probe F10 is used in RFLP analysis of chicken erythrocyte-derived
CC      cDNA. It corresponds to a MHC class I antigen and was obtained from
CC      the total mRNA of different tissues of chicken.
SQ      See also N80602 and N82429.
SQ      Sequence 345 AA.

Query Match
Best Local Similarity 41.0%; Score 97; DB 1; Length 345;
Matches 16; Conservative 8; Mismatches 12; Indels 3; Gaps 3

Db      161 pkkrweeseperrk-nyleetcewllrry-veygxae 197
       | : : : : | | | | | : | : | | | | : | : |
QY      164 PDAANYNDINDVKRLKPGYLEAT-VDMERRRYKVPDGKPE 201

RESULT  4
ID      R42426 standard; Protein; 350 AA.
AC      R42426.
DT      24-MAY-1994 (first entry)
DE      Bovine rod transducin.
KM      Taste modifying agent; ligand; antiligand; binding activity; taste;
KN      taste receptor cells; sweet; bitter; salty; sour; gustducin.
OS      Bos taurus.
PN      MO9321337-A.
PD      28-OCT-1993.
PF      08-APR-1993; U03279.
PI      09-APR-1992; US-868353.
PA      (MARG/) MARCOLSKEE R F.
PR      Margolskee RF:
PI      WPI: 93-351746/44.
DR      New gustducin alpha subunit protein - used for identifying taste
PT      modifying agents which mimic or inhibit sweet, bitter, salty or
PT      sour tastes
PS      Disclosure: Page 34; 50pp; English.
CC      The sequence is that of bovine rod transducin. The sequence was
CC      compared to that of bovine cone transducin and a rat novel taste
CC      cell specific guanine nucleotide binding protein, gustducin, alpha
CC      subunit. Fragments of the protein possessing at least one ligand/
CC      antiligand are binding activity or immunological property specific to
CC      gustducin are taste modifying agents which can be delivered to
CC      taste receptor cells to modify taste, e.g. mimic or inhibit sweet,
CC      bitter, salty or sour tastes.
CC      See also R42405-36.
SQ      Sequence 350 AA.

Query Match
Best Local Similarity 4.5%; Score 95; DB 8; Length 350;
Matches 20; Conservative 17; Mismatches 23; Indels 5; Gaps 5;

Db      146 dsaaay-isdterivtbgyppteqdvlsrsvxlt-gietqsfik-dlnfrmfvagqr 202
       | : | : | : | : | : | : | : | : | : | : | : | : |
QY      165 DAAVYNINDVKRL-KPGYLEATVDWR-RYKVPDGRPENEFAMFNAFKDFADIIKS 222

Db      203 erkfw 207
       | : |
QY      223 THDHW 227

RESULT  5
ID      R42424 standard; Protein; 354 AA.
AC      R42424.
DT      24-MAY-1994 (first entry)
DE      Rat gustducin alpha subunit.
KM      Taste modifying agent; ligand; antiligand; binding activity; taste;
KN      taste receptor cells; sweet; bitter; salty; sour.
OS      Rattus norvegicus.
PN      MO9321337-A.
PD      28-OCT-1993.

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CC disorders by modulating one or more inorganic ion receptor
CC activities; preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 1079 AA;

Query Match          4.2%; Score 90; DB 28; Length 1079;
Best Local Similarity 33.3%; Pred. No. 3.19e+01;
Matches 19; Conservative 16; Mismatches 17; Indels .5; Gaps 5

Db      231 ecdicid-fsellisqgsdeekigqvveiqnstaivvfssgpdleplikeivrr 286
OY      23 NEKGQVISPFD-IPYADKDFHMYVEVRMSNAKMEIA-TKDP-LNP-IKDYVK 75

RESULT  11
ID       W38272 standard; Protein; 1085 AA.
AC       W38272;
DT       08-MAY-1998 (first entry).
DE       Bovine parathyroid cell calcium receptor 1 (BoPCar 1).
KW       Bovine parathyroid cell calcium receptor 1; BoPCar 1;
        calcium homeostasis; hyperparathyroidism; osteoporosis.
OS       Bos sp.
PN       US568938-A.
PD       18-NOV-1997.
PF       07-JUN-1995; 485588.
PR       07-JUN-1995; US-485588.
PR       23-AUG-1991; US-749451.
PR       11-FEB-1992; US-834044.
PR       21-AUG-1992; US-934161.
PR       12-FEB-1993; US-017127.
PR       23-FEB-1993; US-009389.
PR       22-OCT-1993; US-141248.
PR       19-AUG-1994; US-292827.
PR       21-OCT-1994; WO-012117.
PR       08-DEC-1994; US-353784.
PA       (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA       (NNSP-) NPS PHARM INC.
PI       Brown EM, Fuller FH, Garrett JE, Hebert SC,
DR       WPJr; 98-008040/01.
DR       N-PSDB; T95857.
PT       DNA encoding calcium receptor polypeptide(s) - useful for
PT       therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS       Claim 4; Columns 107-116; 174bp; English.
CS       The present sequence is bovine parathyroid cell calcium
CC       receptor 1 (BoPCar 1).
CC       The specification includes details of molecules that can modulate
CC       one or more inorganic ion receptor activities, and antibodies and
CC       antibody fragments targeted to inorganic ion receptor proteins. The
CC       proteins, nucleic acids and antibodies may be used to treat
CC       disorders by modulating one or more inorganic ion receptor
CC       activities; preferably disorders of calcium homeostasis, e.g.
CC       hyperparathyroidism and osteoporosis.
SQ       Sequence 1085 AA;

Query Match          4.2%; Score 89; DB 28; Length 1085;
Best Local Similarity 33.3%; Pred. No. 3.78e+01;
Matches 19; Conservative 16; Mismatches 17; Indels 5; Gaps 5;

Db      232 ecdicid-fsellisqgsdeekigqvveiqnstaivvfssgpdleplikeivrr 287
OY      23 NEKGQVISPFD-IPYADKDFHMYVEVRMSNAKMEIA-TKDP-LNP-IKDYVK 75

RESULT  12
ID       R92524 standard; Protein; 138 AA.
AC       R92524;
DT       12-JUL-1996 (first entry).
DE       Pyridictium occultum DNA polymerase gene PCR product.
KW       DNA pol.; base pair; thermally stable; exonuclease activity;
        polymerase chain reaction; ds.
OS       Pyridictium occultum DSM2709.
FH       Key Location/Qualifiers
FT       misc difference 134
```

/note=" corresponds to ATC codon in T16277"

FT J07327684-A.
 PN 19-DEC-1995.
 PD 09-JUN-1994; 150591.
 PR 09-JUN-1994; JP-150591.
 PA (TAKI) TAKARA SHUZO CO LTD.
 DR WPI: 96-072342/08.
 PT DNA encoding DNA polymerase - useful for prodn. of thermally stable enzyme.
 PS Disclosure: Page 13; 23pp; Japanese
 CC R92524 and R92525 are proteins encoded by amplification products of a PCR performed on Pyrodicticum occultum chromosomal DNA. Two full length genes encoding a 914 amino acid and an 803 amino acid DNA polymerase were later identified. The genes are derived from Pyrodicticum occultum and produce thermostable DNA polymerase. Also disclosed are CC DNA polymerase genes which hybridise to the above genes.
 SQ Sequence 138 AA;

Query Match 4.1%; Score 88; DB 17; Length 138;
 Best Local Similarity 21.6%; Pred. No. 4,47e+01;
 Matches 11; Conservative 15; Mismatches 24; Indels 1; Gaps 1;

Db 3 ypsilrtw-nlsyevtnpyesklvaydvghkvcmsipgltsglqvl 52
 Y 94 YGAIPTWEDPGHNDKHTGCCGNDPIDVCEISKVCAREIIGVAVGL 144

RESULT 13
 ID P70590 standard; protein: 337 AA.
 AC P70590;
 DT 10-APR-1991 (first entry)
 DE Sequence of the human histocompatibility antigen HLA B27.
 KW Rheumatic disorder; genetic screening; diagnosis;
 KM Ankylosing spondylitis.
 OS Homo sapiens.
 PN DE3542024-A.
 PD 04-JUN-1987.
 PF 28-NOV-1985; 542024.
 PR 28-NOV-1985; DE-542024.
 PA (BEHM) BEHRINGWERKE AG.
 PI Riettmuller G, Meo T, Weiss E, Szots H;
 DR WPI: 87-157893/23.
 DR N-PSDB; N70935.
 PT DNA coding for antigen HLA B27 - and diagnostic reagents conty.
 PS Such DNA, antigen or antibody
 CC The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, eg for assessing susceptibility to rheumatic disorders CC such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 CC antibody in human serum, or to produce mono- or polyclonal HLA B27 CC antibodies for use in immunoassay.
 SQ Sequence 337 AA;

Query Match 4.1%; Score 87; DB 2; Length 337;
 Best Local Similarity 24.1%; Pred. No. 5,28e+01;
 Matches 13; Conservative 15; Mismatches 22; Indels 4; Gaps 4;

Db 125 lnedlssvtaadtaagltgr-kweaarvaegqlra-ylegcewllrry-leng 175
 Y 147 IDEGTDKRVIAINVDPPDAANVNDINDVKRLKPGYLEAT-VDWFRYKVPDCK 199

RESULT 14
 ID P70155 standard; protein: 362 AA.
 AC P70155;
 DT 10-MAR-1993 (revised)
 DR 03-APR-1991 (first entry)
 DE Sequence encoded by genomic DNA encoding human histocompatibility antigen HLA-B 27.
 KW Ankylosing spondylitis; rheumatic disorder; diagnosis.
 OS Homo sapiens.

PN EP-226069-A.
 PD 24-JUN-1987.
 PE 21-NOV-1986; 116139.
 PR 01-JAN-1985; DE-542024.
 PR 21-DEC-1985; DE-545576.
 PA (BEHM) BEHRINGWERKE AG.
 PI Szots H, Weiss E, Dörner C, Lang M, Meo T, Riettmuller G;
 DR WPI: 87-171465/25.
 DR N-PSDB; N70225.
 PT DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.
 PS Disclosure: p6; 13pp; German.
 CC The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to CC determine HLA-B 27 levels in human serum, eg for diagnosis of CC rheumatic disorders, esp. ankylosing spondylitis.
 SQ Sequence 362 AA;

Query Match 4.1%; Score 87; DB 3; Length 362;
 Best Local Similarity 24.1%; Pred. No. 5,28e+01;
 Matches 13; Conservative 15; Mismatches 22; Indels 4; Gaps 4;

Db 150 lnedlssvtaadtaagltgr-kweaarvaegqlra-ylegcewllrry-leng 200
 Y 147 IDEGTDKRVIAINVDPPDAANVNDINDVKRLKPGYLEAT-VDWFRYKVPDCK 199

RESULT 15
 ID R12466 standard; protein: 366 AA.
 AC R12466;
 DT 29-AUG-1991 (first entry)
 DE HLA-C exon Cb-2.
 KW Human leukocyte antigen; probe; major histocompatibility complex;
 KM HMC; class I.
 OS Homo sapiens.
 PN J03112485-A.
 PD 14-MAY-1991.
 PF 22-SEP-1989; 247695.
 PR 22-SEP-1989; JP-247695.
 PA (OLYU) OLYMPUS OPTICAL KK.
 DR WPI: 91-182989/25.
 DR N-PSDB; Q12117.
 PT HLA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.
 PS Claim 4; Page 2; 13pp; Japanese.
 CC Probes comprising part of the DNA sequence encoding the protein can CC be used to identify Class I genes. The DNA can be expressed for CC immunisation of animals and prodn. of monoclonal antibodies specific CC for the HLA-C antigen. See also R12465 (same patent) and J03112486 CC and J03112487.
 SQ Sequence 366 AA;

Query Match 4.1%; Score 88; DB 3; Length 366;
 Best Local Similarity 55.0%; Pred. No. 4,47e+01;
 Matches 11; Conservative 6; Mismatches 1; Indels 2; Gaps 2;

Db 182 aylegtcwllrry-leng 200
 Y 181 GYLEAT-VDWFRYKVPDCK 199

Search completed: Thu Sep 17 16:52:03 1998
 Job time : 146 secs.

M O S E R H
(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Sep 17 16:57:21 1998; Maspar time 3.93 Seconds
Tabular output not generated. 518.696 Million cell updates/sec

Title: >US-08-741-437-1
Description: (1-289) from US08741437.dep
Perfect Score: 2134
Sequence: 1 MSGFSTERAAPSLERYRF.....CESACVPTDVKRFHOKN 289

Scoring table: PAM 150
Gap 11

Searched: 77021 segs, 7058996 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfillset1

Statistics: Mean 31.457; Variance 133.821; scale 0.235

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1035	48.5	286	2	PCT-US95-1	Sequence 3, Applicatio	2.04e-89
2	185	8.7	176	2	PCT-US95-1	Sequence 10, Applicati	2.28e-07
3	165	7.7	179	2	PCT-US95-1	Sequence 7, Applicatio	1.23e-05
4	154	7.2	164	2	PCT-US95-1	Sequence 6, Applicatio	1.07e-04
5	111	7.1	263	2	PCT-US95-1	Sequence 4, Applicatio	1.91e-02
6	118	5.5	175	2	PCT-US95-1	Sequence 5, Applicatio	1.45e+00
7	103	4.8	182	1	US-08-127-	Sequence 146, Applicat	2.06e+00
8	101	4.7	182	1	US-08-127-	Sequence 14, Applicati	5.83e+00
9	95	4.5	350	1	US-07-868-	Sequence 15, Applicati	4.14e+00
10	97	4.5	354	1	US-07-868-	Sequence 142, Applicat	9.73e+00
11	92	4.3	182	1	US-08-127-	Sequence 162, Applicat	9.73e+00
12	92	4.3	182	1	US-08-127-	Sequence 161, Applicat	9.73e+00
13	92	4.3	182	1	US-08-127-	Sequence 160, Applicat	9.73e+00
14	92	4.3	182	1	US-08-127-	Sequence 140, Applicat	9.73e+00
15	92	4.3	182	1	US-08-127-	Sequence 147, Applicat	9.73e+00
16	92	4.3	182	1	US-08-127-	Sequence 159, Applicat	9.73e+00
17	92	4.3	182	1	US-08-127-	Sequence 157, Applicat	9.73e+00
18	92	4.3	182	1	US-08-127-	Sequence 144, Applicat	9.73e+00
19	92	4.3	182	1	US-08-127-	Sequence 156, Applicat	9.73e+00
20	92	4.3	182	1	US-08-127-	Sequence 172, Applicat	9.73e+00
21	92	4.3	182	1	US-08-127-	Sequence 173, Applicat	9.73e+00
22	92	4.3	182	1	US-08-127-	Sequence 143, Applicat	9.73e+00
23	92	4.3	182	1	US-08-127-	Sequence 143, Applicat	9.73e+00

24	92	4.3	182	1	US-08-127-	Sequence 137, Applicat	9.73e+00
25	90	4.2	182	1	US-08-127-	Sequence 156, Applicat	1.36e+01
26	90	4.2	182	1	US-08-127-	Sequence 158, Applicat	1.36e+01
27	90	4.2	182	1	US-08-127-	Sequence 135, Applicat	1.36e+01
28	90	4.2	182	1	US-08-127-	Sequence 164, Applicat	1.36e+01
29	89	4.2	182	1	US-08-127-	Sequence 153, Applicat	1.61e+01
30	89	4.2	182	1	US-08-127-	Sequence 145, Applicat	1.61e+01
31	90	4.2	354	1	US-07-868-	Sequence 12, Applicati	1.36e+01
32	90	4.2	375	2	PCT-US93-0	Sequence 8, Applicatio	1.36e+01
33	90	4.2	1079	1	US-08-484-	Sequence 8, Applicatio	1.36e+01
34	90	4.2	1085	1	US-08-485-	Sequence 5, Applicatio	1.61e+01
35	90	4.2	1085	1	US-08-485-	Sequence 5, Applicatio	1.61e+01
36	89	4.2	1085	1	US-08-485-	Sequence 5, Applicatio	1.61e+01
37	89	4.2	1085	1	US-08-485-	Sequence 5, Applicatio	1.61e+01
38	89	4.2	1085	1	US-08-485-	Sequence 5, Applicatio	1.61e+01
39	88	4.1	182	1	US-08-127-	Sequence 138, Applicat	1.91e+01
40	88	4.1	182	1	US-08-127-	Sequence 139, Applicat	1.91e+01
41	88	4.1	182	1	US-08-127-	Sequence 171, Applicat	1.91e+01
42	88	4.1	182	1	US-08-127-	Sequence 170, Applicat	1.91e+01
43	88	4.1	535	1	US-08-455-	Sequence 49, Applicati	2.25e+01
44	87	4.1	1088	1	US-08-484-	Sequence 6, Applicatio	2.25e+01
45	87	4.1	1088	1	US-08-484-	Sequence 6, Applicatio	2.25e+01

ALIGNMENTS

RESULT 1 PCT-US95-13662A-3 STANDARD; PRT: 286 AA.

xxxxxxx

Sequence 3, Application PC/TUS9513662A

Sequence 3, Application PC/TUS9513662A

GENERAL INFORMATION:
APPLICANT: LENNOX, Tricia L.
APPLICANT: SLATKOW, Barton E.
APPLICANT: SEARS, Lauren E.

TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD

CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA

ZIP: 01915

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13662A

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,721

FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.

REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-105-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-1705

TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids

CC

```

CC TELEPHONE: (508) 927-5054
CC TELEFAX: (508) 927-1705
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 176 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 176 AA; 20659 MW; 160121 CN;
Db Query Match 8.7%; Score 185; DB 2; Length 176;
Best Local Similarity 36.9%; Pred. No. 2.28e-07;
Matches 31; Conservative 20; Mismatches 30; Indels 3; Gaps
Qy 116 DNDPDIACEISKVCAREIIGVAVLSILANIDEGEDKVIATNDPDAANTINDV 175
Db 126 -P-KA-FLDEIAHFFORKYELQK 146
Qy 176 KRLKPGYLEATVDWFRRYKVPDQK 199
RESULT 3 STANDARD; PRT; 179 AA.
ID PCT-US95-13662A-7
XX xxxxxx
XX DT
XX DE
XX Sequence 7, Application PC/TUS9513662A
XX Sequence 7, Application PC/TUS9513662A
CC GENERAL INFORMATION:
CC APPLICANT: LENNOX, Tricia L.
CC APPLICANT: SLATKO, Barton E.
CC APPLICANT: SEARS, Lauren E.
CC TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
CC TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
CC NUMBER OF SEQUENCES: 28
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: NEW ENGLAND BIOLABS, INC.
CC STREET: 32 TOZER ROAD
CC CITY: BEVERLY
CC STATE: MASSACHUSETTS
CC COUNTRY: USA
CC ZIP: 01915
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/13662A
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/329,721
CC FILING DATE: 25-OCT-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILKINS, GREGORY D.
CC REGISTRATION NUMBER: 30901
CC REFERENCE/DOCKET NUMBER: NEB-105-PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (508) 927-5054
CC TELEFAX: (508) 927-1705
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 179 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown

```

CC MOLECULE TYPE: protein
SQ SEQUENCE 179 AA; 20465 MW; 177070 CN;
Query Match 7.7%; Score 165; DB 2; Length 179;
Best Local Similarity 30.5%; Pred. No. 1.23e-05;
Matches 32; Conservative 31; Mismatches 38; Indels 4; Gaps 3;
DB 67 DGDPMADVILISOPTFGAIAKVRPIGMKMYVDGETDNKILAVFDKDPNVS-Y--IKDL 123
116 DNDPIDVCEISKVCARGEIIGVAVGLIAMIDGETDMKVIAINVDPPDANNDINDV 175
DB 124 KDVAHLLDELAFNFSTYKIIIEKKTLYLGWEGKALKLEVS 168
OY 176 KRLKGYLEATVDWFRRYKVPDGRKPENEFAFNA-EFKDKDFALDI 219
RESULT 4
ID PCT-US95-13662A-6 STANDARD; PRT: 164 AA.
AC xxxxxx
DE Sequence 6, Application PC/TUS9513662A
XX
CC GENERAL INFORMATION:
CC APPLICANT: LENNOX, Tricia L.
CC APPLICANT: SLATKO, Barton E.
CC APPLICANT: SEARS, Lauren E.
CC TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
CC TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
CC NUMBER OF SEQUENCES: 28
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NEW ENGLAND BIOLABS, INC.
CC STREET: 32 TOZER ROAD
CC CITY: BEVERLY
CC STATE: MASSACHUSETTS
CC COUNTRY: USA
CC ZIP: 01915
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/13662A
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/329,721
CC FILING DATE: 25-OCT-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILLIAMS, GREGORY D.
CC REGISTRATION NUMBER: 30901
CC REFERENCE/DOCKET NUMBER: NEB-105-PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (508) 927-5054
CC TELEFAX: (508) 927-1705
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 164 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
SQ SEQUENCE 164 AA; 18792 MW; 129342 CN;
Query Match 7.2%; Score 154; DB 2; Length 164;
Best Local Similarity 33.3%; Pred. No. 1.07e-04;
Matches 28; Conservative 18; Mismatches 35; Indels 3; Gaps 1;

DB 56 DGDPLDILVITNPFGCVIDIRVIGLYANVDSGEEDAKLIGVVEDP---REDEYRSI 112
116 DNDPIDVCEISKVCARGEIIGVAVGLIAMIDGETDMKVIAINVDPPDANNDINDV 175
DB 113 EDLPQHLKEIAHFERYKIDGR 136
OY 176 KRLKGYLEATVDWFRRYKVPDGR 199
RESULT 5
ID PCT-US95-13662A-4 STANDARD; PRT: 263 AA.
AC xxxxxx
DE Sequence 4, Application PC/TUS9513662A
XX
CC GENERAL INFORMATION:
CC APPLICANT: LENNOX, Tricia L.
CC APPLICANT: SLATKO, Barton E.
CC APPLICANT: SEARS, Lauren E.
CC TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
CC TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
CC NUMBER OF SEQUENCES: 28
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NEW ENGLAND BIOLABS, INC.
CC STREET: 32 TOZER ROAD
CC CITY: BEVERLY
CC STATE: MASSACHUSETTS
CC COUNTRY: USA
CC ZIP: 01915
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/13662A
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/329,721
CC FILING DATE: 25-OCT-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILLIAMS, GREGORY D.
CC REGISTRATION NUMBER: 30901
CC REFERENCE/DOCKET NUMBER: NEB-105-PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (508) 927-5054
CC TELEFAX: (508) 927-1705
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 263 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
SQ SEQUENCE 263 AA; 29712 MW; 339305 CN;
Query Match 7.1%; Score 151; DB 2; Length 263;
Best Local Similarity 37.1%; Pred. No. 1.91e-04;
Matches 23; Conservative 18; Mismatches 21; Indels 0; Gaps 0;
DB 102 CEDSPMDVILVMEPVLTGSEFLARATGLMPMIDOGKDKITAYACADDEFRYRDIK 161
OY 114 GGDNDPIDVCEISKVCARGEIIGVAVGLIAMIDGETDMKVIAINVDPPDANNDINDV 173
DB 162 EL 163
OY 174 DV 175

RESULT 6
ID PCT-US95-13662A-5 STANDARD; PRT: 175 AA.
XX xxxxxx
DT
XX
Sequence 5, Application PC/TUS9513662A
DE
XX
Sequence 5, Application PC/TUS9513662A
CC
GENERAL INFORMATION:
CC APPLICANT: LENNOX, Tricia L.
CC APPLICANT: SLATKO, Barton E.
CC APPLICANT: SEARS, Lauren E.
CC TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
CC TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
CC NUMBER OF INVENTION: LITORALIS
CC NUMBER OF SEQUENCES: 28
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NEW ENGLAND BIOLABS, INC.
CC STREET: 32 TOZER ROAD
CC CITY: BEVERLY
CC STATE: MASSACHUSETTS
CC COUNTRY: USA
CC ZIP: 01915
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/13662A
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/329,721
CC FILING DATE: 25-OCT-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILLIAMS, GREGORY D.
CC REGISTRATION NUMBER: 30901
CC REFERENCE/DOCKET NUMBER: NEB-105-PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (508) 927-5054
CC TELEFAX: (508) 927-1705
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 175 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC SEQUENCE 175 AA; 19572 MW; 155266 CN;
SQ
Query Match 5.5%; Score 118; DB 2; Length 175;
Best Local Similarity 32.2%; Pred. No. 9.80e-02;
Matches 28; Conservative 20; Mismatches 33; Indels 6; Gaps 6;
Db 65 DGDVDV-LVPTPYLPQSGVIRCPVGLKMTDEAGDAKLVAVPHSKL-SKEYDHTKD 122
QY 116 DNDPIDVCEIGSKVCAR-GEIIGVKVLGILAMIDSEGTMKYIAINVDPPDAANTINDIND 174
Db 123 VMDL-PELLKAQIAHFEHYKLENGK 148
QY 175 VKRLKRGYLEATVD-WFRRYK-VPDGK 199
RESULT 7
ID US-08-127-954-165 STANDARD; PRT: 182 AA.
XX xxxxxx
XX

DT
XX
Sequence 165, Application US/08127954
DE
XX
Sequence 165, Application US/08127954
CC
Patent No. 5451512
CC
GENERAL INFORMATION:
CC APPLICANT: Apple, Raymond J.
CC APPLICANT: Bugawan, Teodorica L.
CC APPLICANT: Erlich, Henry A.
CC TITLE OF INVENTION: Methods and Reagents for HLA Class I A
CC TITLE OF INVENTION: Locus DNA Typing
CC NUMBER OF SEQUENCES: 173
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Hoffmann-La Roche Inc.
CC STREET: 340 Kingsland Street
CC CITY: Nutley
CC STATE: New Jersey
CC COUNTRY: U.S.A.
CC ZIP: 07110-1199
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/127,954
CC FILING DATE:
CC CLASSIFICATION: 436
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Petty, Douglas A.
CC REGISTRATION NUMBER: 35,321
CC REFERENCE/DOCKET NUMBER: 8873
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 814-2977
CC TELEFAX: (510) 814-2974
CC INFORMATION FOR SEQ ID NO: 165:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 182 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 182 AA; 21175 MW; 151183 CN;
SQ
Query Match 4.8%; Score 103; DB 1; Length 182;
Best Local Similarity 25.9%; Pred. No. 1.45e+00;
Matches 14; Conservative 17; Mismatches 19; Indels 4; Gaps 4;
Db 126 LNEDLRSWTADMAAQLTOR-KMETAHAEQOLRA-YIEGTCVEYLRKY-LENGK 176
QY 147 IDEGETDMKYIAINVDPPDAANTINDINDVKRLKRGYLEAT-VWFRRYKVPDGK 199
RESULT 8
ID US-08-127-954-146 STANDARD; PRT: 182 AA.
XX xxxxxx
XX
DT
XX
Sequence 146, Application US/08127954
DE
XX
Sequence 146, Application US/08127954
CC
Patent No. 5451512
CC
GENERAL INFORMATION:
CC APPLICANT: Apple, Raymond J.
CC APPLICANT: Bugawan, Teodorica L.
CC APPLICANT: Erlich, Henry A.
CC TITLE OF INVENTION: Methods and Reagents for HLA Class I A
CC TITLE OF INVENTION: Locus DNA Typing
CC NUMBER OF SEQUENCES: 173
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Hoffmann-La Roche Inc.
CC STREET: 340 Kingsland Street
CC CITY: Nutley
CC STATE: New Jersey
CC COUNTRY: U.S.A.
CC ZIP: 07110-1199
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/127,954
CC FILING DATE:
CC CLASSIFICATION: 436
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Petry, Douglas A.
CC REGISTRATION NUMBER: 35,321
CC REFERENCE/DOCKET NUMBER: 8873
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 814-2974
CC TELEFAX: (510) 814-2977
CC INFORMATION FOR SEQ ID NO: 146:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 182 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 182 AA; 21058 MW; 149365 CN;

Query Match 4.7%; Score 101; DB 1; Length 182;
Best Local Similarity 24.1%; Pred. No. 2,06e+00;
Matches 13; Conservative 17; Mismatches 20; Indels 4; Gaps 4;

DB 126 LNEIDRSTADMAQITKR-KWEAHEAEQJRA-YLGGTCVEMLRRL-LENGK 176
QY 147 IDEGETDKVAINVDPPDPAANYNDINDVKRLKPGYLEAT-VDMPFRRYKVPDGK 199

RESULT 9 STANDARD: PRT; 350 AA.
ID US-07-868-353A-14
AC xxxxxx
XX
XX
DT
DE Sequence 14, Application US/07868353A
XX Sequence 14, Application US/07868353A
CC Patent No. 5688662
CC GENERAL INFORMATION:
CC APPLICANT: Margolskee, Robert F.
CC TITLE OF INVENTION: Gustducin Materials and Methods
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESS: Bicknell
CC STREET: Two First National Plaza, 20 South Clark
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/868,353A
CC FILING DATE: 19920409
CC CLASSIFICATION: 530

CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5688662and, Greta E.
CC REGISTRATION NUMBER: P-35,302
CC REFERENCE/DOCKET NUMBER: 28038/30793
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 346-5750
CC TELEFAX: (312) 984-9740
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 350 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 350 AA; 39965 MW; 627049 CN;

Query Match 4.5%; Score 95; DB 1; Length 350;
Best Local Similarity 30.8%; Pred. No. 5.83e+00;
Matches 20; Conservative 17; Mismatches 23; Indels 5; Gaps 5;

DB 146 DSAGYV-LSDERLVTPGYPTEODVLRSRVKT-GIETQFSRK-DLNFEMFDVGGRS 202
QY 165 DAANTNDINDVKRL-KPGYLAIVDWFR-RYKVPDGKPFNEFAFNAEKDXDFALDIIRK 222
DB 203 ERKKV 207
QY 223 THDHW 227

RESULT 10 STANDARD: PRT; 354 AA.
ID US-07-868-353A-15
AC xxxxxx
XX
XX
DT
DE Sequence 15, Application US/07868353A
XX Sequence 15, Application US/07868353A
CC Patent No. 5688662
CC GENERAL INFORMATION:
CC APPLICANT: Margolskee, Robert F.
CC TITLE OF INVENTION: Gustducin Materials and Methods
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESS: Bicknell
CC STREET: Two First National Plaza, 20 South Clark
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/868,353A
CC FILING DATE: 19920409
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5688662and, Greta E.
CC REGISTRATION NUMBER: P-35,302
CC REFERENCE/DOCKET NUMBER: 28038/30793
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 346-5750
CC TELEFAX: (312) 984-9740
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 354 amino acids

Query Match	4.3%;	Score 92;	DB 1;	Length 182
Best Local Similarity	27.7%;	Pred. No.	9.73e+00;	

DT
XX

CC NAME: Petry, Douglas A.
 CC REGISTRATION NUMBER: 35, 321
 CC REFERENCE/DOCKET NUMBER: 8873
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (510) 814-2974
 CC TELEFAX: (510) 814-2977
 CC INFORMATION FOR SEQ ID NO: 140:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 182 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 SQ SEQUENCE 182 AA; 21161 MW; 161123 CN;

Query Match 4.3%; Score 92; DB 1; Length 182;
 Best Local Similarity 27.7%; Pred. No. 9.73e+00;
 Matches 13; Conservative 13; Mismatches 17; Indels 4; Gaps 4;

DB 133 WTADMAAQTKH-KWEAAHYAEQLRA-YLEGTCVEMLRRY-LENGK 176
 Oy 154 WKVIAINVDPPDAANYNDINVKRLKPGYLEAT-VDNFRRYKVPDGR 199

Search completed: Thu Sep 17 16:57:40 1998
 Job time : 19 secs.

100

Asp, Lys, Tyr, Lys #label ASA
#length 383 #molcou1ar-wicbt 31041 #sheekwum 5403

Asp, Lys, Tyr, Lys #label ASA
#length 383 #molcou1ar-wicbt 31041 #sheekwum 5403


```

162-165      #region turn (type I)\
178-181      #region turn (type II)\
204-207      #region turn (type II)\
237-240      #region turn (type II)\
247-250      #region turn (type I)\
250-253      #region turn (type I)\
273-276      #region turn (type I)\
273-278      #region turn (type I)\
SUMMARY      #length 282 #molecular-weight 31781 #checksum 830

Query Match      48.4% Score 1032: DB 5: Length 282:
Best Local Similarity 52.8% Pred. No. 5.83e-166:
Matches 150; Conservative 58; Mismatches 68; Indels 8; Gaps 7;

Db 2 YTRQIGAKNTLEKXVYIEND-GKPSAFHDIPYADKNNIEMVVEIPMTNAKLEIT 60
4 FSTERAPAPSLERVLKNEKGOYISPHDIPYADK--VFIMVVEYERMSAKKEIA 61
61 KEETLNFITDITAKGKIREYRNCPEPHGYIHNGAFQWEDPNVSHPETRKAGDNDPID 120
62 TKPPLNFKODVKKGLRYVYANLEFPYKGYIMWYGAIPQWEDPQHNDRKHGCGCDNDPID 121
Db 121 VLEIGETIATGQVKQKALGIMALLDEGETDMKVIAIDINDPLAPRLNIDYEKTFPG 180
122 VCEIGSVKVCARGELIGVGLIAMDGETDMKVIAINDDDPAANYINDVRLKPG 181
Db 181 LLRATNEMFRIKIPDKPENOFASFGEAKKKYALDIKETHSQKQLAGSSDSKGI 240
182 YLETVYMFRRYKPKDKPEREFNFNAEFKDKDAIDIIKSTHDMKALVT-KITNGKI 240
Db 241 DLATNVLDPTR-TYSKASDAIPPA-SPKAD-A-PIDKSIDKMF 280
241 SCWMTLSESEPKCDPPAARALVDALPPCESACTVPTDVKMF 284
OY

RESULT 7
ENTRY      #type complete
TITLE      inorganic pyrophosphatase (EC 3.6.1.1), chain A - yeast
PDB TITLE  (Saccharomyces cerevisiae)
ORGANISM   acid anhydride hydrolase
REFERENCE  #formal_name Saccharomyces cerevisiae
AUTHORS     Harutyunyan, E.H.; Kuranova, I.P.; Lamzin, V.S.; Dauter, Z.;
            Wilson, K.S.
SUBMISSION #submitted to the Brookhaven Protein Data Bank, May 1996
REFERENCE  #cross-references PDB:1YPP
AUTHORS     Harutyunyan, E.H.; Kuranova, I.P.; Vainshtein, B.K.; Hoehne,
            W.E.; Lamzin, V.S.; Dauter, Z.; Teplyakov, A.V.; Wilson,
            K.S.
JOURNAL    Eur. J. Biochem. (1996) 239:220
TITLE      X-ray structure of yeast inorganic pyrophosphatase complexed
            with manganese and phosphate.
REFERENCE  TN001409
AUTHORS     Harutyunyan, E.H.; Oganessyan, V.Yu.; Oganessyan, N.N.;
            Terzyan, S.S.; Popov, A.N.; Rubinsky, S.V.; Vainshtein,
            B.K.; Nazarova, T.I.; Kurilova, S.A.; Vorobyova, N.N.;
            Ayaeva, S.M.
JOURNAL    Crystallogr. Rep. (Transl. Kristallografiya) (1996) 41:84
TITLE      Structure of inorganic pyrophosphatase from e. coli and its
            complex with a mn2+ ion at 2.2 angstroms resolution.
REFERENCE  TN001410
AUTHORS     Helkimo, P.; Salminen, T.; Lahti, R.; Cooperman, B.;
            Goldman, A.
JOURNAL    Acta Crystallogr. (1995) D51:399
TITLE      New crystal forms of escherichia coli and saccharomyces
            cerevisiae soluble inorganic pyrophosphatases.
REFERENCE  TN001411
AUTHORS     Teplyakov, A.; Oboolova, G.; Wilson, K.S.; Ishii, K.; Kaji,
            H.; Samejima, T.; Kuranova, I.
JOURNAL    Protein Sci. (1994) 3:1098
TITLE      Crystal structure of inorganic pyrophosphatase from thermus
            thermophilus.

REFERENCE  TN001412
AUTHORS     Kankare, J.; Neal, G.S.; Salminen, T.; Glunhoff, T.;
            Cooperman, B.S.; Lahti, R.; Goldman, A.
JOURNAL    Protein Eng. (1994) 7:823
TITLE      The structure of e. coli soluble inorganic pyrophosphatase at
            2.7 a resolution.
REFERENCE  TN001413
AUTHORS     Baykov, A.A.; Shestakov, A.S.
JOURNAL    Eur. J. Biochem. (1992) 206:463
TITLE      Two pathways of pyrophosphate hydrolysis and synthesis by
            yeast inorganic pyrophosphatase.
REFERENCE  TN001414
AUTHORS     Chirgadze, N.Yu.; Kuranova, I.P.; Nevskaya, N.A.; Teplyakov,
            A.V.; Wilson, K.S.; Strokopytov, B.N.; Harutyunyan, E.H.;
            Hoehne, W.E.
JOURNAL    Kristallografiya (1991) 36:128
TITLE      Crystal structure of mmp1 complex of yeast inorganic
            pyrophosphatase at 2.35 angstroms resolution (Russian).
REFERENCE  TN001415
AUTHORS     Kuranova, I.P.; Smirnova, E.A.; Chirgadze, N.Yu.
JOURNAL    Kristallografiya (1990) 35:1581
TITLE      The growing of crystals of inorganic pyrophosphatase from
            yeast with metal ions and phosphate (Russian).
REFERENCE  TN001416
AUTHORS     Kuranova, I.P.; Sokolov, V.I.
JOURNAL    Bioorg. Khim. (1986) 12:749
TITLE      A conformational hypothesis of the trans-ligation of metals
            which activate pyrophosphatase and related enzymes
            (Russian).
REFERENCE  TN001417
AUTHORS     Terzyan, S.S.; Voronova, A.A.; Smirnova, E.A.; Kuranova,
            I.P.; Nekrasov, Yu.V.; Harutyunyan, E.G.; Vainshtein, B.K.;
            Hoehne, W.; Hansen, G.
JOURNAL    Bioorg. Khim. (1984) 10:1469
TITLE      Inorganic pyrophosphatase from yeast at 3 a resolution
            (Russian).
REFERENCE  TN001418
AUTHORS     Knight, W.B.; Dunaway-mariano, D.; Ransom, S.C.; Villafranca,
            J.J.
JOURNAL    J. Biol. Chem. (1984) 259:2886
TITLE      Investigations of the metal ion-binding sites of yeast
            inorganic pyrophosphatase.
REFERENCE  TN001419
AUTHORS     Cooperman, B.S.
JOURNAL    Meth. Enzymol. (1982) 87:526
TITLE      The mechanism of action of yeast inorganic pyrophosphatase.
REFERENCE  TN001420
AUTHORS     Baykov, A.A.; Ayaeva, S.M.
JOURNAL    Eur. J. Biochem. (1974) 47:57
TITLE      Yeast inorganic pyrophosphatase: studies on metal binding.
COMMENT    Resolution: 2.4 angstroms
KEYWORDS   Determination: X-ray diffraction
            hydrolyase
FEATURE    38-40      #region helix (right hand 3-10)\
            64-66      #region helix (right hand 3-10)\
            165-167      #region helix (right hand 3-10)\
            171-177      #region helix (right hand alpha)\
            183-191      #region helix (right hand alpha)\
            194-196      #region helix (right hand 3-10)\
            204-207      #region helix (right hand 3-10)\
            212-231      #region helix (right hand alpha)\
            150-160,133-140,      #region beta barrel\
            42-49,92-95,      #region beta barrel\
            116-123      #region beta barrel\
            150-160,133-140,      #region beta barrel\
            42-49,99-101,      #region beta barrel\
            116-123      #region beta barrel\
            150-160,133-140,      #region beta barrel\
            42-49,34-36      #region beta sheet\
            150-160,141-147,      #region beta sheet\
            202-204      #region beta sheet\
            56-60,67-73,76-76      #region beta sheet\

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56-60, 67-73, 16-22, #region beta sheet\
 1-8, 265-267, #region beta sheet\
 24-26, 16-22, 1-8, #region beta sheet\
 82-84, 278-280 #region beta sheet\
 38-41 #region turn (type I)\
 63-66 #region turn (type II)\
 159-162 #region turn (type I)\
 162-165 #region turn (type II)\
 178-181 #region turn (type II)\
 204-207 #region turn (type II)\
 237-240 #region turn (type II)\
 247-250 #region turn (type I)\
 250-253 #region turn (type I)\
 1-276 #region turn (type I)\
 1-278 #region turn (type I)\
 #length 282 #molecular-weight 31781 #checksum 830

Query Match 48.4%; Score 1032; DB 5; Length 282;
 Best Local Similarity 52.8%; Pred. No. 5,836-166; Indels 8; Gaps 7;
 Matches 150; Conservative 58; Mismatches 68; Indels 8; Gaps 7;

Db 2 YTTTQIGAKNTLEKYKIEKD-GKPSAFHDIPLYADKNNIENNVLEIPMTNKLKLEIT 60
 4 FSTEEERAAFPSTLEKRYELKNEKGOYISPHDIPYADKO--VFHMVVEYPRMSNAKMEIA 61
 Db 61 KEETLNPITIDTAKKGLRVNCFPHHGYIHNAGAFQOTWEDPNVNSHETKAVGNDPID 120
 62 TRDPLNPIDQVAKGKLRVYANLEPKGYIWNAGALPOTWEDBGHDKHCCGDDPID 121
 Db 121 VEIGETIAYTGQVKVAKKLMALDEGETDMKVAINDPLAPKLNDIEDVEKYPFG 180
 122 VCGTSGKVCARGELIGVGLIAMDGEETDMKVAIINVDPPDANYNIDNVKRLKAG 181
 Db 181 LRAINEMFRIRYIPDGKPEPNQAFSGEAKNKYALDIKEHDSKOLIAKSSDSKCI 240
 182 YLEATVDWFRYKVPDGKPEPNQAFSGEAKNKYALDIKEHDSKOLIAKSSDSKCI 240
 Db 241 DLTNVLPDTP-TYSKASDAIPPA-SPKAD-A-PIDKSIDKWF 280
 241 SCNNLTLESFPCDDPARAIVDALPPCESACTVPTDVKWF 284

RESULT 8
 ENTRY 8
 TITLE PWKL #type complete
 inorganic pyrophosphatase (EC 3.6.1.1) - yeast (*Kluyveromyces*
 marxianus var. *lactis*)
 ORGANISM #formal_name *Kluyveromyces marxianus* var. *lactis*, *Candida*
sphaerica
 DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
 05-Sep-1997

ACCESSIONS S07894
 REFERENCE S07892
 #authors Stark, M.J.R.; Milner, J.S.
 #journal Yeast (1989) 5:35-50
 #title Cloning and analysis of the *Kluyveromyces lactis* TRP1 gene: a
 chromosomal locus flanked by genes encoding inorganic
 pyrophosphatase and histone H3.
 #cross-references W01D:89189093
 #accession S07894
 #molecule_type DNA
 #residues 1-287 #label STA
 #cross-references EMBL:X14230; NID:G2900; FID:G2903

GENETICS
 #gene ITP
 CLASSIFICATION #superfamily inorganic pyrophosphatase
 KEYWORDS hydrolyase
 FEATURE
 79, 151 #active_site Arg, Glu #status predicted
 SUMMARY #length 287 #molecular_weight 32165 #checksum 3660

Query Match 47.9%; Score 1022; DB 1; Length 287;
 Best Local Similarity 51.7%; Pred. No. 4,706-164;

Matches 149; Conservative 65; Mismatches 63; Indels 11; Gaps 10;

Db 1 MS-YTTTQVAKNSLDKYYIEKD-GKPSAFHDIPLYADKNNIENNVLEIPMTNKLKLEIT 58
 1 MSGSTERRAAPSTLEKRYELKNEKGOYISPHDIPYADKO--VFHMVVEYPRMSNAKMEIA 58
 Db 59 EITKEEPLNPITIDTAKKGLRVNCFPHHGYIHNAGAFQOTWEDPNVNSHETKAVGNDPID 118
 59 EIAKPDPLNPIDQVAKGKLRVYANLEPKGYIWNAGALPOTWEDBGHDKHCCGDDPID 118
 Db 119 PLDYLEIGEVAATGQVKVAKKLMALDEGETDMKVAINDPLAPKLNDIEDVEKYPFG 178
 119 PIDVCEISKVCARGELIGVGLIAMDGEETDMKVAIINVDPPDANYNIDNVKRLKAG 177
 Db 179 L-PELLATNEMFRIRYIPDGKPEPNQAFSGEAKNKYALDIKEHDSKOLIAKSSDSKCI 237
 178 LKPYLATVDWFRYKVPDGKPEPNQAFSGEAKNKYALDIKEHDSKOLIAKSSDSKCI 236

Db 238 AKKIDLTNTLSDTA-TYSKASDAIPPA-SPKAD-A-PIDKSIDKWF 281
 237 GKGISCAANTLESFPCDDPARAIVDALPPCESACTVPTDVKWF 284

RESULT 9
 ENTRY 9
 TITLE ITPP #type complete
 inorganic pyrophosphatase (EC 3.6.1.1) - yeast (*Saccharomyces*
cerevisiae)
 ORGANISM #formal_name *Saccharomyces cerevisiae*
 #authors Harutyunyan, E.H.; Terzyan, S.S.; Vainshtein, B.K.
 #submision Submitted to the Brookhaven Protein Data Bank, February 1983
 #cross-references PDB:1TPP
 REFERENCE
 #authors Arutunyan, E.G.; Terzyan, S.S.; Voronova, A.A.; Kuranova,
 I.P.; Smirnova, E.A.; Vainshtein, B.K.; Hoehne, W.E.; Hansen,
 G.
 Dokl. Akad. Nauk SSSR (1981) 258:1481
 X-ray diffraction study of inorganic pyrophosphatase from
 baker's yeast at the 3 angstroms resolution (Russian).
 TNO16963
 REFERENCE
 #authors Arutunyan, E.G.; Terzyan, S.S.; Voronova, A.A.; Kuranova,
 I.P.; Smirnova, E.A.; Vainshtein, B.K.; Hoehne, W.E.; Hansen,
 G.
 Dokl. Biochem. (1981) 258:189
 X-ray structural investigation of inorganic pyrophosphatase
 from baker's yeast at 3 angstroms resolution.
 TNO16964
 REFERENCE
 #authors Makhalidiani, V.V.; Smirnova, E.A.; Voronova, A.A.; Tovbis,
 A.B.; Kuranova, I.P.; Harutyunyan, E.G.; Vainshtein, B.K.;
 Bienenwald, B.; Hansen, G.; Hoehne, W.E.
 Kristallografiya (1980) 25:280
 X-ray structural investigation of inorganic pyrophosphatase
 of baker yeast. II. phase calculation and structure model
 at 6 angstroms resolution (Russian).
 TNO16965
 REFERENCE
 #authors Makhalidiani, V.V.; Smirnova, E.A.; Voronova, A.A.; Tovbis,
 A.B.; Kuranova, I.P.; Arutunyan, E.G.; Vainshtein, B.K.;
 Bienenwald, B.; Hansen, G.; Hoehne, W.E.
 Sov. Phys. Crystallogr. (1980) 25:163
 X-ray structural investigation of inorganic pyrophosphatase
 of yeasts. II. calculation of phases and structural model
 at 6 angstroms resolution.
 TNO16966
 REFERENCE
 #authors Smirnova, E.A.; Makhalidiani, V.V.; Voronova, A.A.; Kuranova,
 I.P.; Harutyunyan, E.G.; Vainshtein, B.K.; Heilmann, P.;
 Hoehne, W.E.
 Kristallografiya (1980) 25:104
 X-ray structural investigation of inorganic pyrophosphatase
 of baker yeast. I. Growing of crystals, production of
 derivatives and determination of the heavy atom positions
 in them (Russian).
 TNO16967
 REFERENCE
 #authors Smirnova, E.A.; Makhalidiani, V.V.; Voronova, A.A.; Kuranova,


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Oy 62 TKDPLNPKODVKKGLRYVANLEPPYKGYIMNYGAIPOTWEDPGHNDKHTCCGSDNDPID 121
Db 121 VLEIGETIATYGOVKQVAKALIGIMALLDEGETDMKVIATIDINDPLAPKINDIEDEYKFPG 180
Oy 122 VCEISKVCARGEIIGVAVLIGILAMIDEGEDMKVIATINVDPPDAANNNDINDVKRLKPG 181
Db 181 LIRATNEFRIRYKIPDGKPEKNOFAFGSEAKKKKVALDIKETHDSWKOLINGS 234
Oy 182 YLEATVDWFRYKVPDGRKPEKNEFAFNAEFKDKFAIDIIKSTHDMKALVTKKT 235

RESULT 11
ENTRY S11496 #type complete
TITLE Inorganic pyrophosphatase (EC 3.6.1.1) - fission yeast
ALTERNATE_NAMES (Schizosaccharomyces pombe)
ORGANISM #formal_name Schizosaccharomyces pombe
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
08-Sep-1997

ACCESSIONS S11496
REFERENCE S11496
#authors Kawasaki, I.; Adachi, N.; Ikeda, H.
#journal Nucleic Acids Res. (1990) 18:5888
#title Nucleotide sequence of S. pombe inorganic pyrophosphatase.
#cross_references MUID:91016938
#accession S11496
#molecule_type DNA
#residues 1-289 ##label KAW
#cross_references EMBL:X54301; NID:95013; PID:95014

GENETICS
#gene PPA
#classification #superfamily inorganic pyrophosphatase
KEYWORDS hydrolase
FEATURE
#length 289 #molecular_weight 32467 #checksum 5076
SUMMARY #active_site Arg #status predicted

Query Match 44.58; Score 950; DB 2; Length 289;
Best Local Similarity 48.68; Pred. No. 2,34e-150;
Matches 140; Conservative 66; Mismatches 72; Indels 10; Gaps 9;

Db 1 MSETTREVVALTLDOVVEKN-GTPISWDHIDPLVANAETILINVAEIPRWTOAKL 59
Oy 1 MSGFTSEERAPPSLEFRVFLKNEKQYISPFHDIPITV--DKDVHMYVEVPRMSNAMA 58
Db 60 EITKEATLNDIKODTKKGLRFVNCPPHGIYIWTGAPQIYEDNVVHPETKAGSDS 119
Oy 59 EIAKTDPLNDIKODVKKGLRYVANLEPPYKGYIMNYGAIPOTWEDPGHNDKHTCCGSDND 118
Db 120 PLDYCEIGEARGT-GQVKQVKVIGVALLDEGETDMKVIATIDINDPLAPKINDIEDEYR 178
Oy 119 PIDVCEIG-SKVCARGEIIGVAVLIGILAMIDEGEDMKVIATINVDPPDAANNNDINDVKR 177
Db 179 HMPGLIRATNEFRIRYKIPDGKPEKNOFAFGSECKNRKRYAEVRECNEMERLITKTDPA 238
Oy 178 LKPGYLEATVDWFRYKVPDGRKPEKNEFAFNAEFKDKFAIDIIKSTHDMKALVTKKTNG 237
Db 239 KSDSESLVAVSVGTVAN-DSVVSSTIPPA-QEL-APA-PVDPVSYHKWF 282
Oy 238 KG-ISCNMTTLESFPKCDPDARAIVDALPPOESACTVPTDVKWF 284

RESULT 12
ENTRY A40867 #type complete
TITLE Inorganic pyrophosphatase (EC 3.6.1.1) precursor,
mitochondrial - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein YMR156.09; protein YMR267w
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 27-Mar-1993 #sequence_revision 27-Mar-1992 #text_change
06-Feb-1998
ACCESSIONS A40867
REFERENCE A40867
#authors Lundin, M.; Baltscheffsky, H.; Ronne, H.

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#journal J. Biol. Chem. (1991) 266:12168-12172
#title Yeast PPA2 gene encodes a mitochondrial inorganic
pyrophosphatase that is essential for mitochondrial
function.
#cross_references MUID:91286226
#accession A40867
#molecule_type DNA
#residues 1-310 ##label LUN
#cross_references GB:M81880; NID:q172222; PID:q172223
#accession S54014
#authors Lye, G.; Churcher, C.M.
#submission submitted to the EMBL Data Library, May 1995
#accession S54479
#molecule_type DNA
#residues 1-310 ##label LYE
#cross_references EMBL:Z49260; NID:q809081; PID:q809090; MIPS:YMR267w
#experimental_source strain AB972

GENETICS
#gene SGD:PPA2; IPP2
#cross_references SGD:S0004880; MIPS:YMR267w
#map_position 13R
#genome nuclear
#classification #superfamily inorganic pyrophosphatase
KEYWORDS hydrolase; mitochondrion
FEATURE
1-30 #domain transit peptide (mitochondrion) #status
predicted #label PMP\
31-310 #product inorganic pyrophosphatase #status predicted
#label MAY

SUMMARY #length 310 #molecular_weight 35572 #checksum 6304

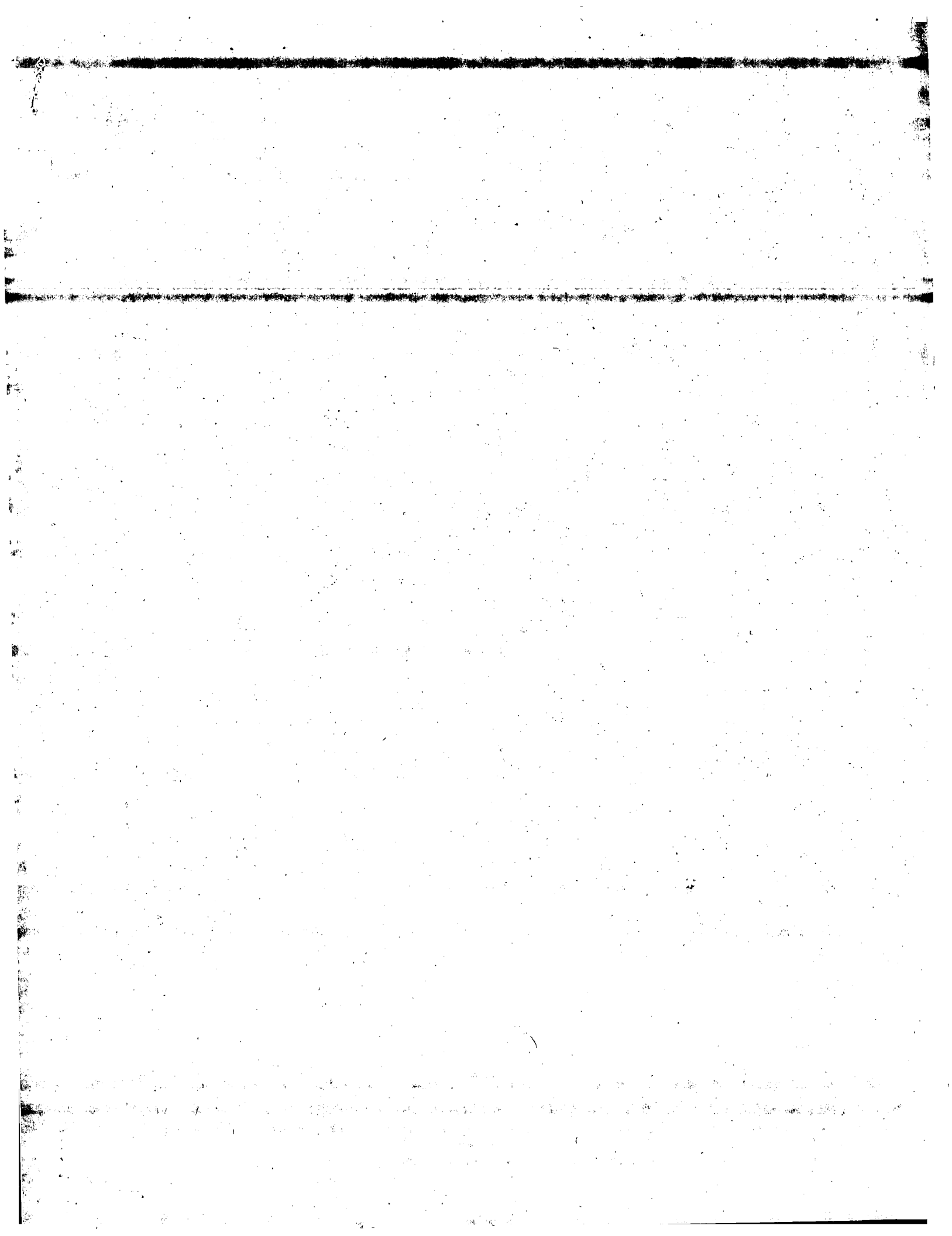
Query Match 38.18; Score 812; DB 2; Length 310;
Best Local Similarity 48.18; Pred. No. 2,99e-124;
Matches 113; Conservative 51; Mismatches 65; Indels 6; Gaps 4;

Oy 4 FSTERAAPSLERVFLVFLKNEKQYISPFHDIPV-YADKP-VHMYVEVPRMSNAMAETA 61
Db 94 KELFNPVVDTKNGKRLFRNNITFPYNGYTHNGAIPQWEDPTIEKLGKGVALKGN 153
Oy 62 TKDPLNPKODVKKGLRYVANLEPPYKGYIWTGALPOTWEDPGHNDKHTCC--GDN 117
Db 154 DPLDCEISDVLDEMGISIKKRVGLSLALIDDELDMKVIATIDINDPLSSKIDLEKIEE 213
Oy 118 DPIDVCEIGSVKCARGEIIGVAVLIGILAMIDEGEDMKVIATINVDPPDAANNNDINDVKR 177
Db 214 YFPGILDTTRKMFYKVPAGKPLNSAFHFOYONSKTIQITKCKNSKNLIS 268
Oy 178 LKPGYLEATVDWFRYKVPDGRKPEKNEFAFNAEFKDKFAIDIIKSTHDMKALVT 232

RESULT 13
ENTRY S29313 #type complete
TITLE Inorganic pyrophosphatase (EC 3.6.1.1) - Thermoplasma
acidophilum
ORGANISM #formal_name Thermoplasma acidophilum
DATE 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change
09-Sep-1997

ACCESSIONS S29313
REFERENCE S29313
#authors Richter, O.M.H.; Schaefer, G.
#journal Eur. J. Biochem. (1992) 209:351-355
#title Cloning and sequencing of the gene for the cytoplasmic
inorganic pyrophosphatase from the thermophilic
archaeobacterium Thermoplasma acidophilum.
#accession S29313
#molecule_type DNA
#residues 1-179 ##label RIC
#cross_references EMBL:X64200; NID:q48081; PID:q48082
KEYWORDS hydrolase
SUMMARY #length 179 #molecular_weight 20465 #checksum 2929

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 M505E1F1 (TM)

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Sep 17 16:53:45 1998; Maspar time 10.59 Seconds
 Tabular output not generated. 684.218 Million cell updates/sec

Title: >US-08-741-437-1
 Description: (1-289) From US08741437.pep
 Perfect Score: 2134
 Sequence: 1 MSGFSTERAPFSLERVF.....CESACTVPTVDKMFHOKN 289

Scoring table: PAM 150
 Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot35
 1:swiss1

Statistics: Mean 47.360; Variance 80.422; scale 0.589

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2063	96.7	289	1	IPYR_BOVIN INORGANIC PYROPHOSPHAT	0.00e+00
2	1035	48.5	286	1	IPYR_YEAST INORGANIC PYROPHOSPHAT	1.47e-213
3	1019	47.8	286	1	IPYR_KLIDIA INORGANIC PYROPHOSPHAT	1.19e-209
4	939	44.0	288	1	IPYR_SCHPO INORGANIC PYROPHOSPHAT	3.83e-190
5	812	38.1	310	1	IPY2_YEAST INORGANIC PYROPHOSPHAT	2.35e-159
6	658	30.8	114	1	IPYR_HUMAN INORGANIC PYROPHOSPHAT	2.02e-122
7	185	8.7	176	1	IPYR_THELI THERMOSTABLE INORGANIC	3.54e-16
8	165	7.7	179	1	IPYR_THEAC INORGANIC PYROPHOSPHAT	2.21e-12
9	154	7.2	164	1	IPYR_BAC3 INORGANIC PYROPHOSPHAT	2.31e-10
10	151	7.1	263	1	IPYR_ARATH SOLUBLE INORGANIC PYRO	8.03e-09
11	149	7.0	173	1	IPYR_SULAC INORGANIC PYROPHOSPHAT	1.83e-09
12	147	6.9	177	1	IPYR_BABA INORGANIC PYROPHOSPHAT	4.16e-09
13	147	6.9	211	1	IPYR_SOLTU SOLUBLE INORGANIC PYRO	4.16e-09
14	125	5.9	184	1	IPYR_MYCPN INORGANIC PYROPHOSPHAT	2.43e-05
15	122	5.7	176	1	IPYR_HAELN PROBABLE INORGANIC PYR	7.51e-05
16	119	5.6	173	1	IPYR_HELPY INORGANIC PYROPHOSPHAT	4.74e-04
17	117	5.5	169	1	IPYR_SYNY3 INORGANIC PYROPHOSPHAT	3.29e-04
18	118	5.5	175	1	IPYR_ECOLI INORGANIC PYROPHOSPHAT	4.74e-04
19	117	5.5	184	1	IPYR_MYGE INORGANIC PYROPHOSPHAT	2.86e-03
20	112	5.2	174	1	IPYR_THERP INORGANIC PYROPHOSPHAT	5.79e-03
21	110	5.0	1102	1	YE20_METUA HYPOTHETICAL PROTEIN M	1.64e-02
22	107	4.9	814	1	CADF_HUMAN MUSCLE-CADHERIN PRECUR	4.56e-02
23	104	4.9	365	1	LA03_GORGO CLASS I HISTOCOMPATIBI	

RESULT ID	1	STANDARD	PRT	289 AA.
AC	P37980;			
DT	01-OCT-1994 (REL. 30, CREATED)			
DT	01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-			
DE	HYDROLASE) (PRASE).			
GN	PP. CHICK			
OS	BOS TAURUS (BOVINE).			
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; ARTIODACTYLA.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE-RETINA;			
RX	MEDLINE: 93077559.			
RA	YANG Z., WENSEL T.G.;			
RL	J. BIOL. CHEM. 267:24641-24647(1992).			
CC	-1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- TISSUE SPECIFICITY: HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER			
CC	SEGMENTS.			
CC	-1- PTM: THE N-TERMINAL IS BLOCKED.			
CC	-1- SIMILARITY: TO OTHER PRASES.			
DR	EMBL: M95283;.. NOT_ANNOTATED_CDS.			
DR	PIR: A45153; A45153.			
DR	HSSP: P00817; IEPY.			
DR	PROSITE: PS00387; PRASE; 1.			
KW	HYDROLASE; MAGNESIUM.			
FT	ACT_SITE 57			
SQ	SEQUENCE 289 AA: 32844 MW: A1D512C4 CRC32:			

ALIGNMENTS

Query Match	Best local Similarity	Score	Pred. No.	Length	Matches	Conservative	Mismatches	Indels	Gaps
Db	1	MSGSSEERAPFTELEYRFLKNEKGOYISPFHDIPYADKEVFHMYVEVPRMSNAKEI	60						
Qy	1	MSGFSTERAPFSLERVFLEKNEKGOYISPFHDIPYADKEVFHMYVEVPRMSNAKEI	60						
Db	61	ATKQPLPIKIDVKKGLRVANFPYKGIYMWGALPQWEDSGHDKRTGCGGNDPI	120						
Qy	61	ATKQPLPIKIDVKKGLRVANFPYKGIYMWGALPQWEDSGHDKRTGCGGNDPI	120						
Db	121	DVCEIGSKVACGEIIRVKVLGILAMIDEGETDMKVAIVNVEDPDAAVNDINDVRLKP	180						

QY 121 DVCISGKVCARGELIGVYGLIAMIDEGELTDMKVIAINVDPDPAANYNDVRLKP 180
 DB 181 GYLEATVDMFRRYVDPGKPENEFAEFAEKDFAIDIESHDYRALVTKTDGKI 240
 QY 181 GYLEATVDMFRRYVDPGKPENEFAEFAEKDFAIDIESHDYRALVTKTDGKI 240
 DB 241 SCMTTISESPFOODPPAAKAIYDALPPCESACTIPTDVKMFHOKN 289
 QY 241 SCMTTISESPFOODPPAAKAIYDALPPCESACTIPTDVKMFHOKN 289
 RESULT 2 STANDARD: PRT: 286 AA.
 ID IPYR YEAST
 AC P00817;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EDARVOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-X2180;
 RX MEDLINE: 89083474.
 RA KOLAKOWSKI L.F. JR., SCHLOSSER M., COOPERMAN B.S.;
 RL NUCLEIC ACIDS RES. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX ZIMMERMAN F.K.;
 RA BAUR A., BOLIS E., MIOSGA T., SCHAEFF-GERSTENSCHLAGER I.,
 RA ZIMMERMAN F.K.;
 RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE.
 RX MEDLINE: 78087552.
 RA COHEN S.A., STERNER R., KEIM P.S., HEINIKSON R.L.;
 RL J. BIOL. CHEM. 253:889-897(1978).
 RN [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN-S288C;
 RX MEDLINE: 95203288.
 RA GARELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,
 RA VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
 RL ELECTROPHORESIS 15:1466-1486(1994).
 RN [5]
 RP SEQUENCE OF 239-249.
 RC STRAIN-ATCC 38531 / Y41;
 RX MEDLINE: 97089742.
 RA NORECK J., BLUMBERG A.;
 RL FEMS MICROBIOL. LETT. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.
 RA BOND M.W., CHIU N.Y., COOPERMAN B.S.;
 RL BIOCHEMISTRY 19:94-102(1980).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA ARUTUNIAN E.G., TERZIAN S.S., VORONOVA A.A., KURANOVA I.P.,
 RA SMIRNOVA E.A., VAINESTEIN B.K., HORNE W.E., HANSEN G.;
 RL DOKL. AKADE. NAUK SSSR 258:1481(1981).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE: 97148342.
 RA HEIKINHEIMO P., LEHTONEN J., BAIKOV A., LAHTI R., COOPERMAN B.S.,
 RL GOLDMAN A.;
 RL STRUCTURE 4:1491-1508(1996).
 RN [9]
 RP SIMILARITY TO E. COLI AND K. LACTIS PPASES.
 RX MEDLINE: 90254161.
 RA LAHTI R., KOLAKOWSKI L.F. JR., HEINONEN J., VIHINEN M., POHJANOKSA K.,
 RA COOPERMAN B.S.;

RL BIOCHIM. BIOPHYS. ACTA 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
 CC CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC IT BINDS UP TO 4 DIVALENT CATIONS PER SUBUNIT, WITH THREE REQUIRED
 CC FOR ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL: X13253; G4199;
 DR EMBL: 235880; G536206;
 DR PIR: S45864; PMBY.
 DR PDB: 1PYP; 15-OCT-91.
 DR PDB: 1YPP; 07-DEC-96.
 DR PDB: 1MGJ; 19-NOV-97.
 DR SWISS-2DPAGE; P00817; YEAST.
 DR YEPD; 7305;
 DR SGD: L0000872; IPPI.
 DR PROSITE: PS00387; PPASE; 1.
 DR KW HYDROLASE; MAGNESIUM; 3D-STRUCTURE.
 FT INIT_MER 0
 FT ACT_SITE 56
 FT BINDING 78
 FT CONFLICT 40
 FT CONFLICT 71
 FT CONFLICT 74
 FT CONFLICT 123
 FT CONFLICT 136
 FT CONFLICT 186
 FT CONFLICT 224
 FT CONFLICT 266
 FT STRAND 4
 FT STRAND 16
 FT STRAND 25
 FT TURN 28
 FT TURN 38
 FT STRAND 45
 FT STRAND 55
 FT STRAND 79
 FT TURN 97
 FT TURN 111
 FT STRAND 121
 FT TURN 131
 FT STRAND 135
 FT STRAND 138
 FT STRAND 151
 FT TURN 160
 FT TURN 165
 FT HELIX 172
 FT TURN 176
 FT TURN 179
 FT HELIX 182
 FT STRAND 203
 FT HELIX 205
 FT STRAND 210
 FT HELIX 212
 FT TURN 231
 FT TURN 245
 FT TURN 248
 FT TURN 251
 FT TURN 255
 FT TURN 274
 SQ SEQUENCE 286 AA; 32184 MW; 0318010F CRC32;
 Query Match 48.5%; Score 1035; DB 1; Length 286;
 Best Local Similarity 53.0%; Pred. No. 1,47e-213;
 Matches 151; Conservative 60; Mismatches 64; Indels 10; Gaps 8;
 DB 2 YTTROIGAKNTLEKRYVIEKD-GKPVSAFHDIPLADKRENNIFNMVVEIPRTNALEIT 60
 QY 4 FSTERAPAFLEKRYVFLKKNKGQYISPFHDIPYADKD-VFHMVVEYPRMSNAKKEIA 61

DB 61 KEETLPIIDOTFKKGLREVRNCFPHHGYTHNCAFPQWEDPNVSHPETKAGVNDPID 120
 QY 62 TDPLPLIKODVKKGLRYVANLEPYKGYIMNGALPQWEDPGHNDKHCGCCGNDPID 121
 DB 121 VLEIGETIAYTGQVKVAKGIMALLDEGETDMKVIAIDINDPLAKLNDIEDVEYFPG 180
 QY 122 VCEIGSKVARGEIIIGVYGLIAMDGETDMKVIAINVDPDAAINYNDINDYKRLKPG 181
 DB 181 LRLATNEMERIKIPGKPNENOFAGSEAKNKKYALDIKETHDSKOLJAGKSSDSKI 240
 QY 182 YLEATVDWFRRYKVPDCKPENEFANAEFKDFAIDIIKSTHDKKALVT-KKTNGKI 240
 DB 241 DLTNTLPTDP-TY-SKAA-S--DAIPPSLKADAPIDSIDKWF 280
 QY 241 SCAMNTLSESPPKCDPDARAIVDALPPEC-ESACTVPTDVDMKF 284

RESULT 3
 ID IPYR_KULUA STANDARD; PRT; 286 AA.
 AC P1398;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 HYDROLASE) (PPEASE).
 GN IPE1 OR IPE.
 OS KLUYVEROMYCES LACTIS (YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 89189093.
 RA STARK M.J.R., MILLER J.S.;
 RL YEAST 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E. COLI AND YEAST PPASES.
 RA MEDLINE; 90254161.
 RA LAHTI R., KOLAKOWSKI L.F. JR., HEINONEN J., VIHINEN M., POHJANOKSA K.,
 RA COOPERMAN B.S.;
 RL BIOCHIM. BIOPHYS. ACTA 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
 CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL; X14230; G2903;
 DR PIR; S07894; PWWK.
 DR HSSP; P00817; IPE.
 DR PROSITE; PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT INIT MET 0
 FT ACT SITE 56
 FT BINDING 78
 FT SEQUENCE 286 AA; 32034 MW; 74833905 CRC32;

Query Match 47.8%; Score 1019; DB 1; Length 286;
 Best Local Similarity 51.4%; Pred. No. 1,19e-209;
 Matches 147; Conservative 66; Mismatches 63; Indels 10; Gaps 9;

DB 1 SYTRVGAKNSLDYVYIEKD-GKPISAFHDIPLYADEANGIFNNVVEIPRTNKLKT 59
 QY 3 GFSTERRAAPSLEVRVFLKNEKGOYISPHDIPYADK-D-VFHHVVEVPRMSNAKMEI 60
 DB 60 TREKPIPIIDOTFKKGLREVRNCFPHHGYTHNCAFPQWEDPNVSHPETKAGVNDPID 119
 QY 61 ATADPLPIKODVKKGLRYVANLEPYKGYIMNGALPQWEDPGHNDKHCGCCGNDPID 120
 DB 120 DYLEIGEOVAAYTGQVKVAKGIMALLDEGETDMKVIAIDINDPLAKLNDIEDVEKHL- 178
 QY 121 DVCETISKVCAREIIIGVYGLIAMDGETDMKVIAINVDPDAAINYNDINDY-KRLK 179
 DB 179 PGLLRATNEMERIKIPGKPNENOFAGSEAKNKKYTLVDVIRSCNEMAKKLGKSDAK 238

QY 180 PGYLEATVDWFRRYKVPDCKPENEFANAEFKDFAIDIIKSTHDKKALVT-KKTNGK 238
 DB 239 KIDLTNTLSDPA-TYSAENASAVPAANLP-DEP--IDKSIDKWF 280
 QY 239 GISCMNTLSESPPKCDPDARAIVDALPPECESACTVPTDVDMKF 284

RESULT 4
 ID IPYR_SCHPO STANDARD; PRT; 288 AA.
 AC P19117;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 HYDROLASE) (PPEASE).
 GN PPA1 OR PPA.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 91016938.
 RA KAWASAKI I., ADACHI N., IKEDA H.;
 RL NUCLEIC ACIDS RES. 18:5888-5888(1990).
 RN [2]
 RP 3D-STRUCTURE MODELLING.
 RA MEDLINE; 92337585.
 RA VIHINEN M., LUNDIN M., BALTSCHIEFSKY H.;
 RL BIOCHIM. BIOPHYS. RES. COMMUN. 186:122-128(1992).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
 CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL; X54301; G5014;
 DR PIR; S11496; S11496.
 DR HSSP; P00817; IPE.
 DR PROSITE; PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT INIT MET 0
 FT ACT SITE 57
 FT BINDING 79
 FT SEQUENCE 288 AA; 32336 MW; DEED9596 CRC32;

Query Match 44.0%; Score 939; DB 1; Length 288;
 Best Local Similarity 48.4%; Pred. No. 3.83e-190;
 Matches 139; Conservative 66; Mismatches 72; Indels 10; Gaps 9;

DB 1 SEYTRREGALNTLDYOYVERKN-GPISSWHDIPLYANAERTILMNVVEIPRTNOKLE 59
 QY 2 GFSTERRAAPSLEVRVFLKNEKGOYISPHDIPYADK-DVDFHVVVEVPRMSNAKME 59
 DB 60 TREKPIPIIDOTFKKGLREVRNCFPHHGYTHNCAFPQWEDPNVSHPETKAGVNDPID 119
 QY 61 ATADPLPIKODVKKGLRYVANLEPYKGYIMNGALPQWEDPGHNDKHCGCCGNDPID 120
 DB 120 DVCETISKVCAREIIIGVYGLIAMDGETDMKVIAINVDPDAAINYNDINDYKRL 178
 QY 121 DYLEIGEOVAAYTGQVKVAKGIMALLDEGETDMKVIAIDINDPLAKLNDIEDVEKHL- 178
 DB 179 PGLLRATNEMERIKIPGKPNENOFAGSEAKNKKYTLVDVIRSCNEMAKKLGKSDAK 238
 QY 239 GISCMNTLSESPPKCDPDARAIVDALPPECESACTVPTDVDMKF 284

RESULT 5
 ID IPY2_YEAST STANDARD; PRT; 310 AA.
 AC P28239;
 DT 01-DEC-1992 (REL. 24, CREATED)

DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE, MITOCHONDRIAL PRECURSOR (EC 3.6.1.1)
 DE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE).
 GN IPP2 OR PPA2 OR YMR267M OR YMR156.09.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA: FUNGI: ASCOMYCOTINA: HEMIASCOMYCETES.
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-W303-1A;
 RX MEDLINE; 91286226.
 RA LUNDIN M., BALTSCHIEFSKY H., RONNE H.;
 RL J. BIOL. CHEM. 266:12168-12172(1991).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA LYE G., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.;
 RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN
 RP 3D-STRUCTURE MODELLING.
 RX MEDLINE; 92357385.
 RA VIHINEN M., LUNDIN M., BALTSCHIEFSKY H.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 186:122-128(1992).
 CC -1- FUNCTION: INVOLVED IN ENERGY PRODUCTION. ITS ACTIVITY IS
 CC STIMULATED BY UNCOUPLERS OF ATP SYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC PROPHOSPHATASE THAT IS ESSENTIAL FOR MITOCHONDRIAL FUNCTION.
 CC -1- SUBUNIT: HOMODIMER THAT BINDS NONCOVALENTLY TO A PROTEIN COMPLEX
 CC IN THE INNER MITOCHONDRIAL MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC
 CC EMBL; M81880; G172223;
 DR EMBL; Z49260; G809090;
 DR PIR; A40867; A40867.
 DR HSSP; P00817; 1PYP.
 DR SCSD; L0001469; PPA2.
 DR PROSITE; PS00387; PPASE, 1.
 KW HYDROLASE, MITOCHONDRION, TRANSIT PEPTIDE.
 FT TRANSIT 1 30
 FT CHAIN 31 310
 FT ACT_SITE 89 89
 FT ACET_SITE 89 89
 FT PROBABLE.
 SQ SEQUENCE 310 AA; 35572 MW; C1DC143B CRC32;
 Query Match 38.1%; Score 812; DB 1; Length 310;
 Best Local Similarity 48.1%; Pred. No. 2,35e-159;
 Matches 113; Conservative 51; Mismatches 65; Indels 6; Gaps 4;

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 RN
 RP SEQUENCE FROM N.A.
 RA LACROIX J., VIGNERON M., KEDINGER C.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC
 CC EMBL; Z48605; G727225;
 DR MIM; 179030;
 DR PROSITE; PS00387; PPASE, 1.
 KW HYDROLASE; MAGNESIUM.
 FT NON_TER 1 114
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 13045 MW; 42DF6303 CRC32;
 Query Match 30.8%; Score 658; DB 1; Length 114;
 Best Local Similarity 72.8%; Pred. No. 2.02e-122;
 Matches 83; Conservative 21; Mismatches 10; Indels 0; Gaps 0;

Db 1 NIPPYGYINNYGTLPTQWEDPEHDKSTNCFGDNPDVCEIGSKILSCGEYHVKLG 60
 Qy 83 NLPYGYINNYGTLPTQWEDPEHDKSTNCFGDNPDVCEIGSKILSCGEYHVKLG 142
 Db 61 TLALIDEGEDWKLAINANDPEASKFHIDYKRRPGYLEATLWFRKYVP 114
 Qy 143 ILAMIDEGEDWKLAINVDDPDANVNDINDYKRLKPGYLEATVDMFRYKVP 196

RESULT 7
 ID IPYR.THELI STANDARD; PRT; 176 AA.
 AC E77992;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE THERMOSTABLE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
 DE PHOSPHO-HYDROLASE) (PPASE).
 GN PPA.
 OS THERMOCOCCUS LITORALIS.
 OC ARCHAEABACTERIA: CRENARCHAEOTA: THERMOPROTEALES; THERMOCOCCACEAE.
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-NS-C;
 RA LENNOX T.L., SEARS L.E., MORAN L.S., SLATKO B.E.;
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 PHOSPHATE.
 CC -1- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC
 CC EMBL; U49440; G1518483;
 DR PROSITE; PS00387; PPASE, 1.
 KW HYDROLASE; MAGNESIUM.
 FT ACT_SITE 30 30
 FT ACET_SITE 30 30
 FT BY SIMILARITY.
 SQ SEQUENCE 176 AA; 20659 MW; 3DB64F1F CRC32;
 Query Match 8.7%; Score 185; DB 1; Length 176;
 Best Local Similarity 36.9%; Pred. No. 3.54e-16;
 Matches 31; Conservative 20; Mismatches 30; Indels 3; Gaps 3;

Db 66 DDDPEIDMVMREFTYGVLIARPGIFGIMISGDKDYKLVAVPDPYFNDKDISDY 125
 Qy 116 DNDPIDVCEIGSKYKARGELIGVAVLGILAMIDEGEDWKLAINVDDPDANVNDINDY 175
 Db 126 -P-KA-FLDELIAHFFORKELOGK 146
 Qy 176 KRLKPGYLEATVDMFRYKVPDKK 199

RESULT 8

ID IPYR.THEAC STANDARD; PRT: 179 AA.
 AC P37981;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 HYDROLASE) (PPASE).
 GN PPA.
 OS THERMOPLASMA ACIDOPHILUM.
 OC ARCHAEABACTERIA; EURYARCHAEOTA; THERMOPLASMALES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DSM 1728.
 RA MEDLINE; 93011147.
 RA RICHTER O.-M.H.; SCHAEFER G.;
 RL EUR. J. BIOCHEM. 209:351-355(1992).
 RN [2]
 RP SEQUENCE OF 1-22. AND CHARACTERIZATION.
 RX MEDLINE; 93011146.
 RA RICHTER O.-M.H.; SCHAEFER G.;
 RL EUR. J. BIOCHEM. 209:343-349(1992).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL: X64200; G48082;
 DR PIR: S29282; S29282.
 DR PIR: S29313; S29313.
 DR HSSP: P17288; 1E1P.
 DR PROSITE: PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT ACT_SITE 31
 FT SEQUENCE 179 AA; 20465 MW; C07397F6 CRC32;
 SO
 Query Match 7.7%; Score 165; DB 1; Length 179;
 Best Local Similarity 30.5%; Pred. No. 2,21e-12;
 Matches 32; Conservative 31; Mismatches 38; Indels 4; Gaps 3;
 DB 67 DGDPMVDVLIISQTPFGAIIKVRPIGMKAVDQGETDNKILAVFDKDPNVY-Y--IKDL 123
 116 DNDPIDVCEIGSKVCAIGELIGVKGILAMIDEGEDMKVIAINVDPPAANYNDINDV 175
 DB 124 KDVAHHLDELAFNEFTYKILEKETKYLGEGEALKEIEVSI 168
 176 KRLKPGYLEATVDMFRRKVPDGRKPEMEFAENA-EFKDKDEAIDI 219
 QY
 RESULT 9
 ID IPYR.EACB3 STANDARD; PRT: 164 AA.
 AC P19514;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 HYDROLASE) (PPASE).
 GN PPA.
 OS BACILLUS PS3 (THERMOPHILIC BACTERIUM PS-3).
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-DSM 1728.
 RA MEDLINE; 91154162.
 RA ICHIBA T.; TAKENAKA O.; SAMEJIMA T.; HACHIMORI A.;
 RL J. BIOCHEM. 108:572-578(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
 CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMOTRIMER. IN PRESENCE OF DIVALENT CATIONS THE TRIMERS
 AGGREGATE TO FORM A HEXAMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR PIR: JX0135; JX0135.
 DR HSSP: P17288; 1E1P.
 DR PROSITE: PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.

FT ACT_SITE 20 20 BY SIMILARITY.
 SQ SEQUENCE 164 AA; 18792 MW; FF88D7C4 CRC32;
 Query Match 7.2%; Score 154; DB 1; Length 164;
 Best Local Similarity 33.3%; Pred. No. 2,31e-10;
 Matches 28; Conservative 18; Mismatches 35; Indels 3; Gaps 1;
 DB 56 DGDPLDILVITTPPPGCVIDTRVIGYLMNVDGSEEDAKLIGVEDP---RFEDEYRSI 112
 116 DNDPIDVCEIGSKVCAIGELIGVKGILAMIDEGEDMKVIAINVDPPAANYNDINDV 175
 DB 113 EDLPQHKLEIAHFFERYKDLQK 136
 176 KRLKPGYLEATVDMFRRKVPDGR 199
 QY
 RESULT 10
 ID IPYR.ARATH STANDARD; PRT: 263 AA.
 AC P21216;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE SOLUBLE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 HYDROLASE) (PPASE).
 GN PPA.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC CAPRALES; CRUCIFERAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE; 91370878.
 RA KIEBER J.J.; SIGNER E.R.;
 RL PLANT MOL. BIOL. 16:345-348(1991).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: ACTIVITY DEPENDENT ON MG2+ (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL: X57545; G16348;
 DR PIR: S13379; S13379.
 DR HSSP: P17288; 1E1P.
 DR PROSITE: PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT ACT_SITE 68
 FT SEQUENCE 263 AA; 29712 MW; F6B4A9E4 CRC32;
 SO
 Query Match 7.1%; Score 151; DB 1; Length 263;
 Best Local Similarity 37.1%; Pred. No. 8,03e-10;
 Matches 23; Conservative 18; Mismatches 21; Indels 0; Gaps 0;
 DB 102 CEQSDPMVDVLIISQTPFGAIIKVRPIGMKAVDQGETDNKILAVFDKDPNVY-Y--IKDL 161
 114 DNDPIDVCEIGSKVCAIGELIGVKGILAMIDEGEDMKVIAINVDPPAANYNDINDV 173
 DB 162 EL 163
 174 DV 175
 QY
 RESULT 11
 ID IPYR.SULAC STANDARD; PRT: 173 AA.
 AC P50308;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 HYDROLASE) (PPASE).
 GN PPA.
 OS SULFOLOBUS ACIDOCALDARIUS.
 OC ARCHAEABACTERIA; CRENARCHAEOTA; SULFOBALES.
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN-DSM 639;

RX MEDLINE: 95289717.
 RA MEYER W., MOLL R., KATH T., SCHAEFER G.;
 RL ARCH. BIOCHEM. BIOPHYS. 319:149-156(1995).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: ABSOLUTE REQUIREMENT FOR MAGNESIUM.
 CC -1- SUBUNIT: HOMOTETRAMER. CYTOPLASMIC.
 CC -1- SUBCELLULAR LOCATION: TO OTHER PPASES.
 DR EMBL: X81842; G886704; -
 DR PROSITE: PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT ACT_SITE 26
 SQ SEQUENCE 173 AA; 19381 MW; 4FAE97B3 CRC32;
 BY SIMILARITY.
 Query Match 7.0%; Score 149; DB 1; Length 173;
 Best Local Similarity 33.7%; Pred. No. 1.83e-09;
 Matches 29; Conservative 22; Mismatches 31; Indels 4; Gaps 4;
 Db 62 DDDPLVLTNTNQLP-GSVIEVRPIGLVKKDEGEDAKIVAVPKDTPS-FSNIKD 119
 QY 116 DNDPIVCEIGS-KVCARGEIIGVGLIAMDSEGTDMKVIALINDDPDANINDIND 174
 Db 120 INDLPQATKKNKIVHFEHFKYKELEPGK 145
 QY 175 VKRLKPGYLEATVDFRRRYKVPD-GK 199
 RESULT 12 STANDARD; PRT; 177 AA.
 ID IPYR-BARBA
 AC P51064;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN PPA.
 OS BARTONELLA BACILLIFORMIS.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; RICKETTSIAS; RICKETTSIALES;
 CC BARTONELLACEAE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-KC583;
 RA MITCHELL S.J., MINNICK M.F.;
 RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
 CC CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY. BINDS 4 DIVALENT
 CC CATIONS PER SUBUNIT (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL: I46591; G940255; -
 DR PROSITE: PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT ACT_SITE 30
 SQ SEQUENCE 177 AA; 20064 MW; 31852443 CRC32;
 BY SIMILARITY.
 Query Match 6.9%; Score 147; DB 1; Length 177;
 Best Local Similarity 30.4%; Pred. No. 4.16e-09;
 Matches 35; Conservative 23; Mismatches 53; Indels 4; Gaps 3;
 Db 66 DSDPIVLCVTRPLIPGCVINVRPIGALIMDDGKGEKIIVPTPL-TOQYIGIDY 124
 QY 116 DNDPIVCEIGSKVCARGEIIGVGLIAMDSEGTDMKVIALINDDPDANINDINDV 175
 Db 125 TDLTENILKKIEHFEHFKY--DLEAGK-WAKIEGWMDKNFARFELLQQAIERAKI 176
 QY 176 KRLKPGYLEATVDFRRRYKVPDCKPENEFARFARFADIKSTHDKWAL 230
 RESULT 13 STANDARD; PRT; 211 AA.
 ID IPYR-SOLTU
 AC Q43187;

DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE SOLUBLE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN PPA.
 OS SOLANUM TUBEROSUM (POTATO).
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 CC SOLANALES; SOLANACEAE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA DU JARDIN P., ROJAS-BELTRAN J., GEBHARDT C., BRASSEUR R.;
 RL PLANT PHYSIOL. 109:853-860(1995).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: ACTIVITY DEPENDENT ON MG2+.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL: Z36894; G534916; -
 DR PROSITE: PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT ACT_SITE 61
 SQ SEQUENCE 211 AA; 24261 MW; 8E8F92C CRC32;
 BY SIMILARITY.
 Query Match 6.9%; Score 147; DB 1; Length 211;
 Best Local Similarity 37.2%; Pred. No. 4.16e-09;
 Matches 32; Conservative 16; Mismatches 35; Indels 3; Gaps 1;
 Db 95 CEDNDPMDVILMOEVLDFGCLLRARATGLMPIDGEGDKIIVACADDPYRHYTDI- 153
 QY 114 CGNDPIVCEIGSKVCARGEIIGVGLIAMDSEGTDMKVIALINDDPDANINDIND 173
 Db 154 --KOLPFRALRIREFEDYKKNK 177
 QY 174 DVKRLKPGYLEATVDFRRRYKVPDCK 199
 RESULT 14 STANDARD; PRT; 184 AA.
 ID IPYR-MYCEN
 AC P75250;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN PPA.
 OS MYCOPLASMA PNEUMONIAE.
 OC PROKARYOTA; TENERICUTES; MOLICUTES; MYCOPLASMA; MYCOPLASMATALES;
 CC MYCOPLASMATACEAE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RA MEDLINE: 97105885.
 RA HIMMELREICH R., HILBERT H., FLAGENS H., PIRKL E., LI B.-C.,
 RA HERMANN R.;
 RL NUCLEIC ACIDS RES. 24:4420-4449(1996).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
 CC CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY. BINDS 4 DIVALENT
 CC CATIONS PER SUBUNIT (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: TO OTHER PPASES.
 DR EMBL: AE000029; G1673987; -
 DR PROSITE: PS00387; PPASE; 1.
 KW HYDROLASE; MAGNESIUM.
 FT ACT_SITE 19
 SQ SEQUENCE 184 AA; 21369 MW; D5F880FD CRC32;
 BY SIMILARITY.
 Query Match 5.9%; Score 125; DB 1; Length 184;
 Best Local Similarity 28.6%; Pred. No. 2.43e-05;
 Matches 18; Conservative 22; Mismatches 20; Indels 3; Gaps 3;

DB 72 GVVVPTRIYVGALEWVDGELDTKLIGV-ID-CDP-RYKEINSVNDLPKRVNDEIGFIKT 128
 OY 133 GEIIGVYKGIILAMIDEGSETDMKVIAINVDDPDANVINDVKKRLKPGYLEATVDFERR 192
 DB 129 YKL 131
 OY 193 YKV 195

RESULT 15

ID IPYR.HAEIN STANDARD: PRT: 176 AA.

AC P44529; 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE PROBABLE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE

DE PHOSPHO-HYDROLASE) (PPASE).

CN PPA OR HI0124.

OS HAEMOPHILUS INFLUENZAE.

OC PROKARYOTA: GRACILICUTES; SCOTOBACTERIA: FACULTATIVELY ANAEROBIC RODS;

OC PASTEURRELLACEAE.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-RD / KW20.

RX MEDLINE: 95350630.

RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

RA KERLAVAGE A.R., BULT C.J., TOMB C.J., DOUGHERTY B.A., MERRICK J.M.,

RA MCKENNEY K., SUTTON G., FITZHIGH W., FIELDS C.A., GOCAYNE J.D.,

RA SCOTT J.D., SHIREY R., LIO L.-I., GLODER A., KELLEY J.M.,

RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,

RA UTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDER D.M., BRANDON R.C.,

RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,

RA GENTH C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,

RA VENTER J.C.;

RL SCIENCE 269:496-512(1995).

CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.

CC -1- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL

CC CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY. BINDS 4 DIVALENT

CC CATIONS PER SUBUNIT (BY SIMILARITY).

CC -1- SUBUNIT: HOMOHEXAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC EMBL: U32698; G1573079; -

DR PROSITE: PS00387; PPASE; 1.

DR TIGR: HI0124; -

KW HYDROLASE; MAGNESIUM.

FT ACT_SITE 31 31 BY SIMILARITY.

SQ SEQUENCE 176 AA; 19725 MW; CEBBD6F CRC32;

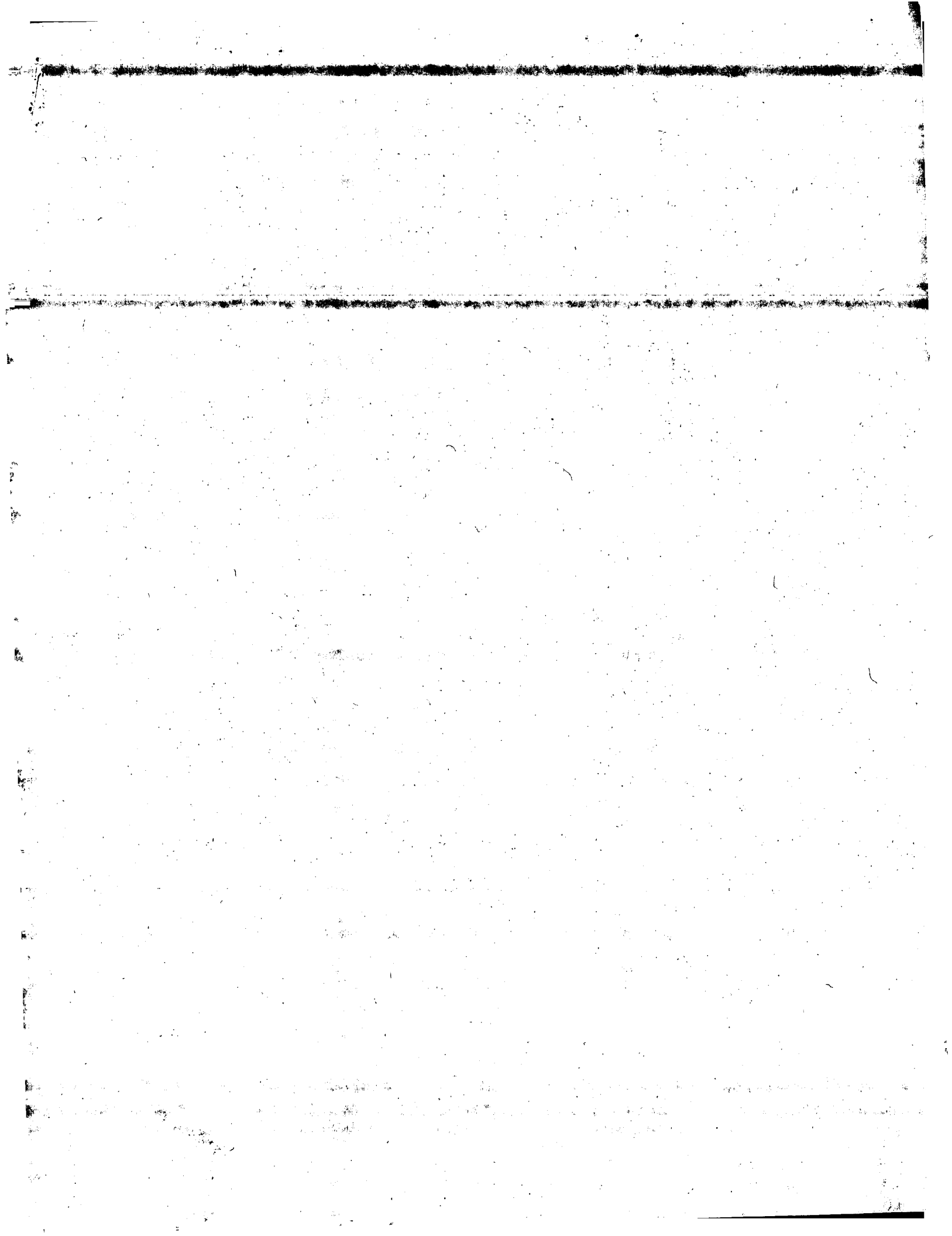
Query Match 5.7%; Score 122; DB 1; Length 176;

Best Local Similarity 29.6%; Pred. No. 7.51e-05;

Matches 34; Conservative 26; Mismatches 46; Indels 9; Gaps 7;

DB 67 DGEDELVLITRPLATGVLEAKVIGVKKFEVDGEVDKIVCPADRDGTGNAYNSIAD 126
 OY 116 DNDPIDVCEIGSKVARGEIIIGVYKGIILAMIDEGSETDMKVIAINVDDPDAN-YNDIND 174
 DB 127 ---L-PAULIKIEFHFNFKYKALK-KPGST-KV-TIMGVVEAKVIRRSIKRW 174
 OY 175 VKRLPGYLEATVDM-FRRYKVPDGKPNENFAFNAEFKDKDFALDIKSTHDMK 228

Search completed: Thu Sep 17 16:54:43 1998
 Job time : 58 secs.





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Msrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Sep 17 16:55:00 1998; Maspar time 18.79 Seconds
647.612 Million cell updates/sec

Tabular output not generated.

Title: >US-08-741-437-1
Description: (1-289) from US08741437.pep
Perfect Score: 2134
Sequence: 1 MSGFSTERAPFSLERYVF.....CESACTVPTDVKMFHQKN 289

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sprenb16
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 46.257; Variance 82.300; scale 0.562

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1119	52.4	292	3	Q18680	HYPOTHETICAL PROTEIN C	6.23e-224
2	1005	47.1	285	1	013505	INORGANIC PYROPHOSPHAT	2.86e-197
3	864	40.5	286	1	P87118	HYPOTHETICAL 32.9 KD P	1.72e-164
4	154	7.2	164	9	005724	PYROPHOSPHATASE (FRAGM	8.78e-10
5	143	6.7	215	9	023979	SOLUBLE INORGANIC PYRO	6.87e-08
6	135	6.3	176	9	026363	INORGANIC PYROPHOSPHAT	1.50e-06
7	126	5.9	136	9	049071	INORGANIC PYROPHOSPHAT	4.35e-05
8	123	5.8	214	8	022537	INORGANIC PYROPHOSPHAT	1.30e-04
9	117	5.5	178	9	034955	INORGANIC PYROPHOSPHAT	1.12e-03
10	108	5.1	363	5	030223	MHC CLASS I ATBE-G*03	2.50e-02
11	109	5.1	482	8	041676	LEGUMIN A PRECURSOR.	1.78e-02
12	106	5.0	356	5	030444	MHC CLASS I CAVA-G*04	4.87e-02
13	107	5.0	357	5	030914	MHC CLASS I A (FRAGMEN	3.49e-02
14	107	5.0	367	5	008680	RT1 CLASS I HISTOCOMPA	3.49e-02
15	107	5.0	377	5	019445	MHC CLASS IB ANTIGEN.	3.49e-02
16	104	4.9	181	5	095409	MHC CLASS I A ANTIGEN	9.45e-02
17	104	4.9	358	5	030593	MHC CLASS I ANTIGEN MA	9.45e-02
18	102	4.8	91	5	035555	(STRAIN BM6) ALPHA-2 D	1.81e-01
19	103	4.8	181	5	029766	MHC TYPE I ANTIGEN (FR	1.31e-01
20	102	4.8	356	5	030445	MHC CLASS I CAVA-G*05	1.81e-01

21	103	4.8	362	5	P79523	MHC CLASS I HISTOCOMPA	1.31e-01
22	103	4.8	1662	9	034313	YEKN PROTEIN.	1.31e-01
23	101	4.7	166	5	095518	HISTOCOMPATIBILITY ANT	2.50e-01
24	101	4.7	166	5	095516	HISTOCOMPATIBILITY ANT	2.50e-01
25	100	4.7	181	5	019354	MHC CLASS I A ANTIGEN	3.45e-01
26	101	4.7	294	5	030714	MHC CLASS I ANTIGEN MA	2.50e-01
27	100	4.7	344	5	P79602	MATURE ALPHA CHAIN OF	3.45e-01
28	100	4.7	354	5	095514	HISTOCOMPATIBILITY ANT	3.45e-01
29	100	4.7	354	5	095513	HISTOCOMPATIBILITY ANT	3.45e-01
30	101	4.7	363	5	019642	MHC CLASS I ANTIGEN HL	2.50e-01
31	101	4.7	363	5	029840	MHC HLA-A*0301 BLANK G	2.50e-01
32	101	4.7	365	5	019756	MHC CLASS I HLA-A.	2.50e-01
33	101	4.7	3063	2	099715	COLLAGEN TYPE XII ALPH	2.50e-01
34	99	4.6	91	5	031189	MHC CLASS I H2-K-ALPHA	4.74e-01
35	99	4.6	91	5	P79617	MHC CLASS I HLA-C (FRA	4.74e-01
36	99	4.6	91	5	019635	MHC CLASS I ANTIGEN HL	4.74e-01
37	99	4.6	181	5	019505	HLA-CW6 (FRAGMENT).	4.74e-01
38	98	4.6	246	5	029945	MHC CLASS I HLA-A CELL	6.49e-01
39	99	4.6	347	4	029505	GALACTOSIDE 2-L-FUCOSY	4.74e-01
40	98	4.6	356	5	030171	LYMPHOCYTE ANTIGEN.	6.49e-01
41	99	4.6	357	5	030917	MHC CLASS I A (FRAGMEN	4.74e-01
42	98	4.6	358	5	030291	MHC CLASS I PRECURSOR.	6.49e-01
43	99	4.6	366	5	029991	HLA CLASS I HEAVY CHAI	4.74e-01
44	99	4.6	366	5	031605	ALPHA CHAIN OF MHC CLA	4.74e-01
45	99	4.6	366	5	029864	HLA-C ALPHA CHAIN PREC	4.74e-01

ALIGNMENTS

RESULT 1
ID Q18680; PRELIMINARY; PRT; 292 AA.
AC Q18680;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN C47E12.4.
GN C47E12.4.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHADITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RA COLES L.
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULLON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIJFEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RL NATURE 368:32-38(1994).
KW EMBL: Z68882; E348322;
DR HYPOTHETICAL PROTEIN.
SQ SEQUENCE 292 AA; 32363 MW; A31DC923 CRC32;

Query Match 52.4%; Score 1119; DB 3; Length 292;
Best Local Similarity 53.2%; Pred. No. 6.23e-224;
Matches 150; Conservatve 65; Mismatches 60; Indels 7; Gaps 6;

DB	11	YEAVERGSLSYSDRYVYIGPOG-IYSPHDIPLFNKDKRYNMVETLPRNTAKMEKA	69
QY	4	FTEERBAAPFSLERYFLKNEGQYISPHDIPYADKO-VFHWVVEPRKSNKMEIA	61
DB	70	TREPSPIKODEKKGVARVNIHIFPKIGIINYGALPOTWEDPNHVPDTAKGNDPID	129
QY	62	TDDPLNPIKOVKKGLRYVAMLPFKYGIWYGAIPQWEDPCHGDKHTGCCNDNDPID	121

Db 130 VIEWSGVARGAVLOVYGLTALIDEGETDMKLVADVDNDENADKLNDIDVYKYPG 189
 122 VCEIGSKVARGELIYGVKGLIAMIIDEGETDMKLVADVDNDENADKLNDIDVYKYPG 181
 Db 190 LLAASWEFNNYIPAGKPANFAENGFEKREKREYAKVDELINENKYLII-KEANP-SLN 247
 182 YLEATVDMFRYKVPDCKPENEFANFAEFKDFALDIIDIKSHDHMKALVYTKTKNGKIS 241
 Db 248 TV-SRVEAVHOGTDEAAATAGATPEHGAN-PLPGDYDKW 287
 242 CMNTLSESPKCDPDAAARALVALPPCHSACTVPTVDKWM 283

RESULT 2
 ID 013505 PRELIMINARY: PRT: 285 AA.
 AC 013505;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (EC 3.6.1.1).
 GN IPII
 OS PICHIA PASTORIS (YEAST).
 OC PLASMID PRS316-GAL1.
 OC EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRL Y-11430.
 RA COSANO I., ALVAREZ P., MOLINA M., NOMBELA C.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ001000; E1180018;
 KW HYDROLASE; PLASMID.
 SQ SEQUENCE 285 AA; 32068 MW; 6D19F407 CRC32;

Query Match 47.1%; Score 1005; DB 1; Length 285;
 Best Local Similarity 52.4%; Pred. No. 2,86e-197;
 Matches 150; Conservative 56; Mismatches 71; Indels 9; Gaps 8;

Db 1 MS-YSTRQIGANTLENRYFIKD-GQVVSPPHDIPLADSKYLVNMYVVPWNTAKL 58
 1 MSFSTEEBAAPPSLEYRFLKNEKQYISPHDIPYAD-KDVEHNVAVEPRNSNKM 58
 Db 59 EISEKELNPIIDOTKKGLRFRVNCFFPHGYIHYNGAFPTWEDPNTHEETAKGND 118
 59 EITKPLNPIKODVKKGLRYANLFPYKGIYMWGAIPQWEDPGNDKHTGCCGND 118
 QY 119 PLVCEIGERSYT-GQVKQYVGVALLDEGETDMKVIIDINDPLAKLNDIDVYK 177
 119 PLVCEIGERSYT-GQVKQYVGVALLDEGETDMKVIIDINDPLAKLNDIDVYK 178
 Db 178 MGLLRATNEMERYIKIPDGKPNQAFSGECKNNKYAEVIOCREAMEKLIIFGKTSPG 237
 179 KPGYLEATVDMFRYKVPDCKPENEFANFAEFKDFALDIIDIKSHDHMKALVYTKTKNG 238
 QY 238 EIDLNTLTISTP-SFSPASAVPTA-SPA-APA-KIDQSIDKWF 279
 239 GISCMNTLSESPKCDPDAAARALVALPPCHSACTVPTVDKWF 284

RESULT 3
 ID P87118 PRELIMINARY: PRT: 286 AA.
 AC P87118;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DE HYPOTHEICAL 32.9 KD PROTEIN.
 GN SPAC3A12.02.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA BADOCK K., CHURCHER C.M.;

RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA WOOD V., BARRELL B.G., RAJANDREAM M.A.;
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 295395; E316097;
 KW HYPOTHEICAL PROTEIN.
 SQ SEQUENCE 286 AA; 32898 MW; E702438D CRC32;

Query Match 40.5%; Score 864; DB 1; Length 286;
 Best Local Similarity 55.5%; Pred. No. 1.72e-164;
 Matches 122; Conservative 40; Mismatches 55; Indels 3; Gaps 3;
 Db 23 DFRVYCYKNNK-P-ISEFDVPLTSKDPFNWTEIPWTOAKCEISLSPFHPKODLK 80
 16 EYRVF-LKNKGOYISPFPHDIPYADKDFHNVVEPRNSNKMELIATKPLNPIKODK 74
 Db 81 NGKLRYVANSFPYHGYIYNGALPQWEDPNVIDSTKMGDGLDVCIGSGIYGI 140
 75 KGLRYVANLFPYKGIYMWGAIPQWEDPGNDKHTGCCGNDPDIVCIGSKVARG 134
 Db 141 IKQVYIAGLIDGSETDMKLIIDINDPRAKLNDISGVONLMPRLPCTRWFAIYK 200
 135 IIGVYGLIAMIIDEGETDMKVIIDINDPDAANYNDINDVYKRLKPGYLEATVDMFRYK 194
 Db 201 IPDGKPNRFFEGNYPKSDALDIIOCHQHWKVS RDK 240
 195 VPDGKPNRFFANFAEFKDFALDIIDIKSHDHMKALVYTK 234

RESULT 4
 ID 005724 PRELIMINARY: PRT: 164 AA.
 AC 005724;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DE PYROPHOSPHATASE (FRAGMENT).
 GN PMK2PPA.
 OS BACILLUS STEAROTHERMOPHILUS.
 OC PROCAROTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 12016;
 RA SATOH T., ISHII K., KOTAMA M., SAKURAI N., KAJI H., HACHIMORI A.,
 RA IRIE M., SAMEJIMA T.;
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB003087; D1020624;
 FT NON_TER 1 164
 SQ SEQUENCE 164 AA; 18796 MW; BD71D735 CRC32;

Query Match 7.2%; Score 154; DB 9; Length 164;
 Best Local Similarity 33.3%; Pred. No. 8.78e-10;
 Matches 28; Conservative 18; Mismatches 35; Indels 3; Gaps 1;
 Db 56 DGGPDIVVTINTPPGVIVRIVGYLWVDSGEADKLGIVVEDP---REDEVERSI 112
 116 DNDPDIVCIGSVARGELIYGVKGLIAMIIDEGETDMKVIIDINDPDAANYNDINDV 175
 QY 113 EDLPQKLEIAHFFERYKDLCK 136
 176 KRLKPGYLEATVDMFRYKVPDCK 199

RESULT 5
 ID 023979 PRELIMINARY: PRT: 215 AA.
 AC 023979;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE SOLUBLE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1).
 GN IIP.

OS HORDEUM VULGARE VAR. DISTICHUM (TWO-ROWED BARLEY).
 OC EUKARYOTAE; MITOCHONDRIAL EUKARYOTES; VIRIDILANTAE;
 OC CHAROPHYTA; EMBRYOPHYTA GROUP; EMBRYOPHYTA; VASCULAR PLANTS;
 OC SEED PLANTS; MAGNOLIOPHYTA; LILLOPSIDA; POALES; POACEAE; HORDEUM;
 OC HORDEUM VULGARE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. TRIUMPH.
 RA VISSER K., HEIMOVARA-DIKSTRA S., KIJNE J.W., WANG M.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF009675; G2258074; -
 KW HYDROLASE.
 SQ SEQUENCE 215 AA; 24049 MW; DF89ED71 CRC32;
 Query Match 6.7%; Score 143; DB 8; Length 215;
 Best Local Similarity 36.4%; Pred. No. 6.87e-08;
 Matches 24; Conservative 18; Mismatches 23; Indels 1; Gaps 1;
 Db 101 CGNDPMDVLTVMQEPITPSSFLRAAIGLMPIDGKDKIIVCADPEYRHSYV 160
 QY 114 CGNDPIDVCEIGSKVCARGELIGVKVILAMIDEGTDMKVIAlNVDDPDANYN-DI 172
 Db 161 SLFRL 166
 QY 173 NDVKRL 178
 RESULT 6
 ID 026363 PRELIMINARY; PRT; 176 AA.
 AC 026363;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE.
 GN MTH263.
 OS METHANOBACTERIUM THERMOCALOTOTROPHICUM.
 OC ARCHAEABACTERIA; EURYARCHAEOTA; METHANOBACTERIALES;
 OC METHANOBACTERIACEAE.
 RN [1]
 GN SEQUENCE FROM N.A.
 RP STRAIN-DELTA H;
 RC SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
 RA ALDERIDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
 RA HARRISON D., HOANG L., KEGGLE P., LUM W., POTTER B., QIU D.,
 RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
 RA JIWANI N., CARISO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
 RA MODOGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
 RA DANIELS C.J., MAO J.-T., RICE P., NOLLING J., REEVE J.N.;
 RL J. BACTERIOL. 179:7135-7153(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RA SMITH D.R.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF000812; G2621313; -
 SQ SEQUENCE 176 AA; 20084 MW; 66900C6C CRC32;
 Query Match 6.3%; Score 135; DB 9; Length 176;
 Best Local Similarity 34.5%; Pred. No. 1.50e-06;
 Matches 29; Conservative 16; Mismatches 36; Indels 3; Gaps 3;
 Db 66 DGDPMDLVLTVMQEPITPSSFLRAAIGLMPIDGKDKIIVCADPEYRHSYV 125
 QY 116 DNDPIDVCEIGSKVCARGELIGVKVILAMIDEGTDMKVIAlNVDDPDANYN-DI 175
 Db 126 -P-EHN-LKEIANFEYKLEK 146
 QY 176 KRLKPGYLEATVDMFRYKVPDGR 199
 RESULT 7
 ID 049071 PRELIMINARY; PRT; 136 AA.
 AC 049071;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE (FRAGMENT).
 OS MYCOPLASMA CAPRICOLUM.
 OC PROKARYOTA; TENERICUTES; MOLICUTES; MYCOPLASMA; MYCOPLASMATALES;
 OC MYCOPLASMATACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 27343(KID);
 RA MEDLINE; 96059641.
 RA BORK P., OUZOUNIS C., CASARI G., SCHNEIDER R., SANDER C., DOLAN M.,
 RA GILBERT W., GILLEMET P.M.;
 RL MOL. MICROBIOL. 16:955-967(1995).
 DR EMBL: Z33286; G530477; -
 FT NON TER 1
 SQ SEQUENCE 136 AA; 15815 MW; 5BF224DC CRC32;
 Query Match 5.9%; Score 126; DB 9; Length 136;
 Best Local Similarity 31.0%; Pred. No. 4.35e-05;
 Matches 26; Conservative 17; Mismatches 38; Indels 3; Gaps 3;
 Db 16 DGDPMDLVLTVMQEPITPSSFLRAAIGLMPIDGKDKIIVCADPEYRHSYV 160
 QY 116 DNDPIDVCEIGSKVCARGELIGVKVILAMIDEGTDMKVIAlNVDDPDANYN-DI 175
 Db 76 -P-KH-YRXXXXXFFLOYKALQNK 96
 QY 176 KRLKPGYLEATVDMFRYKVPDGR 199
 RESULT 8
 ID 022537 PRELIMINARY; PRT; 214 AA.
 AC 022537;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE.
 GN IPP.
 OS ORYZA SATIVA (RICE).
 OC EUKARYOTA; PLANTAE; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
 OC CYPERALES; GRAMINEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MILYANG 23; TISSUE-SEED;
 RA LEE M.C., KIM C.S., EUN M.Y.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF022733; G2570501; -
 SQ SEQUENCE 214 AA; 23610 MW; ED159571 CRC32;
 Query Match 5.8%; Score 123; DB 8; Length 214;
 Best Local Similarity 31.0%; Pred. No. 1.30e-04;
 Matches 31; Conservative 22; Mismatches 39; Indels 6; Gaps 6;
 Db 98 CEDGPMDLVLTVMQEPITPSSFLRAAIGLMPIDGKDKIIVCADPEYRHSYV 125
 QY 114 CGNDPIDVCEIGSKVCARGELIGVKVILAMIDEGTDMKVIAlNVDDPDANYN-DI 173
 Db 157 RKSPTA-FKRSAY-FEEDYKKNENKAVNEF-FPAE 191
 QY 174 DVRLKPGYLEATVDMFRYKVPDGR-E-NEFAFNAE 209
 RESULT 9
 ID 034955 PRELIMINARY; PRT; 178 AA.
 AC 034955;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE INORGANIC PYROPHOSPHATASE.
 GN PPA.
 OS LEGIONELLA PNEUMOPHILA.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;

OC LEGIONELLACEAE.
 RN SEQUENCE FROM N.A.
 RC STRAIN-A100.
 RA ABU KWAIR Y.
 RL INFECT. IMMUN. 66:0-0(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A100.
 RA ABU KWAIR Y.
 RL INFECT. IMMUN. 0:0-0(1997).
 DR EMBL: AF034464; G264227;
 DR EMBL: AF030232; G2613038;
 SQ SEQUENCE 178 AA; 20049 MW; E3505B05 CRC32;
 Query Match 5.5%; Score 117; DB 9; Length 178;
 Best Local Similarity 27.9%; Pred. No. 1,12e-03; Indels 4; Gaps 4;
 Matches 24; Conservative 21; Mismatches 37;
 Db 66 DGDVPLVTPVPLISGVISCRVAGMLKMTDESGVDKILAVPTTKL-SKATQSMQY 124
 OY 116 DNDPIDVCEIGSVKVCARGELITGVGLAMIDEGTDMKVAIVDDPDANINDV 175
 Db 125 ODI-POHLLSTIEHFKNYDLLEEG 149
 OY 176 KRLKPGYLEATVD-WFRRYK-VPDGR 199
 RESULT 10 PRELIMINARY; PRT; 363 AA.
 ID Q30223;
 AC Q30223;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE MHC CLASS I ATBE-G*03 (FRAGMENT).
 GN ATBE-G. BELZERTH (LONG-HAIRED SPIDER MONKEY).
 OS ATBE-G. BELZERTH (LONG-HAIRED SPIDER MONKEY).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CADAVIT L.F.; SHUFFLEBOTHAM C.; RUIZ F.J.; YEAGER M.; HUGHES A.L.;
 RA WATKINS D.I.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U59650; G1389913;
 DR PROSITE: PS00290; IG_MHC. 1.
 KW MHC.
 FT NON_TER 1
 SQ SEQUENCE 363 AA; 40827 MW; 0EA568E CRC32;
 Query Match 5.1%; Score 108; DB 5; Length 363;
 Best Local Similarity 27.3%; Pred. No. 2.50e-02; Indels 4; Gaps 4;
 Matches 15; Conservative 16; Mismatches 20;
 Db 141 VINEDLRSTADVAQAQITQR-KWEANAARMA-YLEGTCEVWLRRY-LENGK 192
 OY 146 MIDGETDMKVAIVDDPDANINDVYKRLKPGYLEAT-VDWFRRYKVPDGR 199
 RESULT 11 PRELIMINARY; PRT; 482 AA.
 ID Q41676;
 AC Q41676;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE LEGUMIN A PRECURSOR.
 OS VICIA NABOBENSIS.
 OC EUKARYOTA; PLANTAE; EMERIOBIONTA; MAGNOLIOPHYTA; MAGNOLIOPSIDA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISUB-COTYLEDON;
 DR NONG V.; BECKER C.; MUENTZ K.;

RL SUBMITTED (NOV-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SUBUNIT: HEXAMER; EACH SUBUNIT IS COMPOSED OF AN ACIDIC AND A
 CC BASIC CHAIN DERIVED FROM A SINGLE PRECURSOR AND LINKED BY A
 CC DISULFIDE BOND (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER 11S SEED STORAGE PROTEINS (GLOBULINS).
 DR EMBL: Z46803; G660108;
 DR PROSITE: PS00305; 11S_SEED_STORAGE; 1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 482 AA; 54667 MW; 901C5103 CRC32;
 Query Match 5.1%; Score 109; DB 8; Length 482;
 Best Local Similarity 32.3%; Pred. No. 1.78e-02; Indels 9; Gaps 8;
 Matches 30; Conservative 21; Mismatches 33;
 Db 138 GDIIAVPTGNVIMTNDQTP--VIAISLTPTGSSN-NOLDQIPR-R-FYLAGNOQEFL 192
 OY 133 GEIIQVYVIGIILAMIDEGTDMKVAIVDDPDANINDVYKRLKPGYLEATVDW-FR 191
 Db 193 RYQREGGKQEOENDGNIFSGFKDFLEDALN 225
 OY 192 RX-KVPDGPENEFANERKD-K-DEAIDILK 221
 RESULT 12 PRELIMINARY; PRT; 356 AA.
 ID Q30444;
 AC Q30444;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 DE MHC CLASS I CAJA-G*04 (FRAGMENT).
 GN CALITRAX JACCHUS (COMMON MARROSET).
 OS CALITRAX JACCHUS (COMMON MARROSET).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CADAVIT L.F.; SHUFFLEBOTHAM C.; RUIZ F.J.; YEAGER M.; HUGHES A.L.;
 RA WATKINS D.I.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U59640; G1389927;
 DR PROSITE: PS00290; IG_MHC. 1.
 KW MHC.
 FT NON_TER 1
 SQ SEQUENCE 356 AA; 39894 MW; ECF4FAE CRC32;
 Query Match 5.0%; Score 106; DB 5; Length 356;
 Best Local Similarity 27.8%; Pred. No. 4.87e-02; Indels 4; Gaps 4;
 Matches 15; Conservative 15; Mismatches 20;
 Db 142 INEDLRSTADVAQAQITQR-KWEANAARMA-YLEGTCEVWLRRY-LENGK 192
 OY 147 IDEGETDMKVAIVDDPDANINDVYKRLKPGYLEAT-VDWFRRYKVPDGR 199
 RESULT 13 PRELIMINARY; PRT; 357 AA.
 ID Q30914;
 AC Q30914;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE MHC CLASS I A (FRAGMENT).
 GN PAN TROGLODYTES (CHIMPANZEE).
 OS PAN TROGLODYTES (CHIMPANZEE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 95279794.
 RA MCADAM S.N.; BOYSON J.E.; LIU X.; GARBER T.L.; HUGHES A.L.;
 RA BONTROP R.E.; WATKINS D.I.;
 RL EMBL: U10539; G506670;
 DR PROSITE: PS00290; IG_MHC. 1.
 KW MHC.

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FT  NON TER      1      1
   SEQUENCE      357 AA; 39890 MM; 24BFILF7 CRC32;

Query Match
Best Local Similarity 27.8%; Score 107; DB 5; Length 357;
Matches 15; Conservative 15; Mismatches 20; Indels 4; Gaps 4;

DB  142 LNEIDRSTADMAAQTQR-KWEAAHAERLRA-YLECTCVEMLRV-LENGK 192
    147 IDEGETDMVIAINVDDPDPAANYNDINDVKRLKPGYLEAT-VDMEFRYKVPDOK 199

RESULT  14
ID  Q08680; PRELIMINARY; PRT; 367 AA.
AC  Q08680;
DT  01-NOV-1996 (TREMBLREL. 01, CREATED)
DT  01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE  01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE  RT1 CLASS I HISTOCOMPATIBILITY ANTIGEN, LM2 ALPHA CHAIN PRECURSOR.
GN  LM2.
OS  RATIUS NORVEGICUS (RAT).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; RODENTIA.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-LEW/GUN; TISSUE-CONA STIMULATED LYMPHOCYTES;
RX  MEDLINE: 94222444.
RA  WALTER L., HEINE L., GUENTHER E.;
RL  IMMUNOGENETICS 39:351-354(1994).
DR  EMBL: X70066; G56610;
KM  MHC I; TRANSMEMBRANE.
FT  SIGNAL 1 21 POTENTIAL.
FT  CHAIN 22 367 RT1 CLASS I HISTOCOMPATIBILITY ANTIGEN,
SQ  SEQUENCE 367 AA; 41053 MM; 60475057 CRC32; LM2 ALPHA CHAIN.

Query Match
Best Local Similarity 27.0%; Score 107; DB 5; Length 367;
Matches 20; Conservative 19; Mismatches 29; Indels 6; Gaps 6;

DB  122 CDVSGSILRGIDQFAIDGRYLALNEDLKT-WMA-ADTAQMTRNKWDQGEARHKA 179
    123 CEIGSKVCA-RG-EIIGKVVLGIAMIDGETDMKVIAINVDDPDPAANYNDINDVKRLK 180
    180 -YLOGTCVEMLRV 192
    181 GYLEAT-VDMEFRY 193

OY  181 GYLEAT-VDMEFRY 193

RESULT  15
ID  019445; PRELIMINARY; PRT; 377 AA.
AC  019445;
DT  01-JAN-1998 (TREMBLREL. 05, CREATED)
DT  01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE  01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE  MHC CLASS IB ANTIGEN.
GN  RT1.CI.
OS  RATIUS NORVEGICUS (RAT).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; RODENTIA.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-LEW;
RX  MEDLINE: 95276971.
RA  LAMBRACHT D., WONIGEIT K.;
RL  IMMUNOGENETICS 41:375-379(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-LEW;
RA  LAMBRACHT D., DUEVEL H., WONIGEIT K.;
RL  SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN  [3]
RP  SEQUENCE FROM N.A.

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RC  STRAIN-LEW;
RA  LAMBRACHT D.;
RL  SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR  EMBL: AF025308; G2570821;
SQ  SEQUENCE 377 AA; 42200 MM; 335C92C1 CRC32;

Query Match
Best Local Similarity 27.0%; Score 107; DB 5; Length 377;
Matches 20; Conservative 19; Mismatches 29; Indels 6; Gaps 6;

DB  122 CDVSGSILRGIDQFAIDGRYLALNEDLKT-WMA-ADTAQMTRNKWDQGEARHKA 179
    123 CEIGSKVCA-RG-EIIGKVVLGIAMIDGETDMKVIAINVDDPDPAANYNDINDVKRLK 180
    180 -YLOGTCVEMLRV 192
    181 GYLEAT-VDMEFRY 193

OY  181 GYLEAT-VDMEFRY 193

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Search completed: Thu Sep 17 16:57:04 1998
Job time : 124 secs.

